

WO 2005/037989

PCT/US2003/024918

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt

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Gln	Lys	Cys	Leu	Gly	Leu	Asp	Ile	Thr	Lys	Ser	Val	Asn	Glu	Leu	Arg
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Met	Phe	Ser	Cys	Asp	Ser	Ser	Ala	Met	Leu	Trp	Trp	Lys	Cys	Glu	His
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His	Ser	Leu	Tyr	Gly	Ala	Ala	Arg	Tyr	Arg	Leu	Ala	Leu	Lys	Asp	Gly
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His	Gly	Thr	Ala	Ile	Ser	Asn	Ala	Ser	Asp	Val	Trp	Lys	Lys	Gly	Gly
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Ser	Glu	Glu	Ser	Leu	Cys	Asp	Gln	Pro	Tyr	His	Glu	Ile	Tyr	Thr	Arg
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160	165	170													
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Cys	Leu	Lys	Pro	Glu	Asn	Gly	Cys	Glu	Asp	Asn	Trp	Glu	Lys	Asn	Glu
190	195	200													
Gln	Phe	Gly	Ser	Cys	Tyr	Gln	Phe	Asn	Thr	Gln	Thr	Ala	Leu	Ser	Trp
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280	285	290													
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295	300	305													
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310	315	320													
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Ala	His	Ala	Lys	Cys	Lys	Ala	Phe	Ser	Ser	Asp	Leu	Ile	Ser	Ile	His
355	360	365													
Ser	Leu	Ala	Asp	Val	Glu	Val	Val	Val	Thr	Lys	Leu	His	Asn	Glu	Asp
370	375	380													
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385	390	395													
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400	405	410													
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445	450	455													
Ser	Asp	Lys	Met	Cys	Pro	Pro	Asp	Glu	Gly	Trp	Lys	Arg	His	Gly	Glu
460	465	470													
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505	510	515													
Arg	Asp	Val	Asp	Ser	Cys	Gly	Glu	Tyr	Asn	Trp	Ala	Thr	Val	Gly	Gly
520	525	530													
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Tyr Lys Val Phe His Ala Glu Arg Ile Val Arg Lys Arg Asn Trp Glu
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Glu Ala Glu Arg Phe Cys Gln Ala Leu Gly Ala His Leu Ser Ser Phe
675 680 685
Ser His Val Asp Glu Ile Lys Glu Phe Leu His Phe Leu Thr Asp Gln
690 695 700
Phe Ser Gly Gln His Trp Leu Trp Ile Gly Leu Asn Lys Arg Ser Pro
705 710 715 720
Asp Leu Gln Gly Ser Trp Gln Trp Ser Asp Arg Thr Pro Val Ser Thr
725 730 735
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740 745 750
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Tyr Glu Glu Ala Val Leu Tyr Cys Ala Ser Asn His Ser Phe Leu Ala
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945 950 955 960
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1090 1095 1100
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1105 1110 1115 1120
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      1585      1590      1595
Gly Leu Ser Gln His Ser Val Asp Gln Ser Trp Ser Trp Leu Asp Gly
      1605      1610      1615
Ser Glu Val Thr Phe Val Lys Trp Glu Asn Lys Ser Lys Ser Gly Val
      1620      1625      1630
Gly Arg Cys Ser Met Leu Ile Ala Ser Asn Glu Thr Trp Lys Lys Val
      1635      1640      1645
Glu Cys Glu His Gly Phe Gly Arg Val Val Cys Lys Val Pro Leu Gly
      1650      1655      1660
Pro Asp Tyr Thr Ala Ile Ala Ile Ile Val Ala Thr Leu Ser Ile Leu
      1665      1670      1675
Val Leu Met Gly Gly Leu Ile Trp Phe Leu Phe Gln Arg His Arg Leu
      1685      1690      1695

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
His Leu Ala Gly Phe Ser Ser Val Arg Tyr Ala Gln Gly Val Asn Glu
1700 1705 1710
Asp Glu Ile Met Leu Pro Ser Phe His Asp
1715 1720

<210> 146
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Exemplary linker.

<400> 146
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10 15

<210> 147
<211> 1518
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse-Human hybrid fusion protein

<400> 147
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ccaggggaga aggtcacaaat gacttgccagg gccagctcaa gtgtaagtta catgcactgg 180
taccagcaga agccaggatc ctccccaaa ccctggattt atgccccatc caacctggct 240
tctggagtcg ctgctcgctt cagtggcagt gggctctggga cctcttactc tctcacaaatc 300
agcagagtgg aggtgaaga tgctgccact tattactgcc agcagtggag ttttaaccca 360
cccacgttcg gtgctgggac caagctggag ctgaaagggt gcggtggctc gggcggtggt 420
ggatctggag gaggtgggag ctctcaggct tatctacagc agtctggggc tgagctgggt 480
aggcctgggg cctcagtga gatgtcctgc aaggcttctg gctacacatt taccagttac 540
aatatgcact gggtaaagca gacacctaga cagggcctgg aatggattgg agctatttat 600
ccaggaaatg gtgatacttc ctacaatcag aagttcaagg gcaaggccac actgactgta 660
gacaaatcct ccagcacagc ctacatgcag ctacagcagc tgacatctga agactctgct 720
gtctatttct gtgcaagagt ggtgtactat agtaactctt actggtactt cgatgtctgg 780
ggcacaggga ccacggtcac cgtctctgat caggagccca aatcttctga caaaactcac 840
acatgccccac cgtgccacg acctgaactc ctgggggggac cgtcagctctt cctcttcccc 900
ccaaaaccca aggacaccct catgatctcc cggacccttg aggtcacatg cgtgggtgggt 960
gacgtgagcc acgaagacc tgagggtcaag ttcaactggt acgtggacgg cgtggagggtg 1020
cataatgccca agacaaagcc gcgggaggag cagtacaaca gcacgtaccg tgtggtcagc 1080
gtcctcaccg tcctgcacca ggactggctg aatggcaagg agtacaagt caaggtctcc 1140
aacaagccc tcccagcccc catcgagaaa acaatctcca aagccaaagg gcagccccga 1200
gaaccacagg tgtacaccct gccccatcc cgggatgagc tgaccaagaa ccaggtcagc 1260
ctgacctgcc tgggtcaaagg cttctatccc agcgacatcg ccgtggagtg ggagagcaat 1320
gggcagccgg agaacaacta caagaccag cctcccgtgc tggactccga cggctccttc 1380
ttcctctaca gcaagctcac cgtggacaag agcaggtggc agcaggggaa cgtcttctca 1440
tgctccgtga tgcatgaggc tctgcacaac cactacacgc agaagagcct ctccctgtct 1500
ccgggtaaat gatctaga 1518

<210> 148
<211> 499
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse-Human hybrid fusion protein

<400> 148
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1 5 10 15
Val Ile Ile Ala Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile
20 25 30
Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser

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Ser	Ser	Val	Ser	Tyr	Met	His	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Ser	Ser
Pro	Lys	Pro	Trp	Ile	Tyr	Ala	Pro	Ser	Asn	Leu	Ala	Ser	Gly	Val	Pro
Ala	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Ser	Tyr	Ser	Leu	Thr	Ile
Ser	Arg	Val	Glu	Ala	Glu	Asp	Ala	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Trp
Ser	Phe	Asn	Pro	Pro	Thr	Phe	Gly	Ala	Gly	Thr	Lys	Leu	Glu	Leu	Lys
Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Ser
Gln	Ala	Tyr	Leu	Gln	Gln	Ser	Gly	Ala	Glu	Leu	Val	Arg	Pro	Gly	Ala
Ser	Val	Lys	Met	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Thr	Ser	Tyr
Asn	Met	His	Trp	Val	Lys	Gln	Thr	Pro	Arg	Gln	Gly	Leu	Glu	Trp	Ile
Gly	Ala	Ile	Tyr	Pro	Gly	Asn	Gly	Asp	Thr	Ser	Tyr	Asn	Gln	Lys	Phe
Lys	Gly	Lys	Ala	Thr	Leu	Thr	Val	Asp	Lys	Ser	Ser	Ser	Thr	Ala	Tyr
Met	Gln	Leu	Ser	Ser	Leu	Thr	Ser	Glu	Asp	Ser	Ala	Val	Tyr	Phe	Cys
Ala	Arg	Val	Val	Tyr	Tyr	Ser	Asn	Ser	Tyr	Trp	Tyr	Phe	Asp	Val	Trp
Gly	Thr	Gly	Thr	Thr	Val	Thr	Val	Ser	Asp	Gln	Glu	Pro	Lys	Ser	Cys
Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly
Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met
Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His
Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val
His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr
Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly
Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile
Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val
Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser
Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu
Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro
Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val
Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met
His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser
Pro	Gly	Lys													

<210> 149

<211> 1470

<212> DNA

<213> Artificial Sequence

<220>

<223> Mouse-Human hybrid fusion protein

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt

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ccaggggaga aggtcacaaat gacttgcagg gccagctcaa gtgtaagtta catgcactgg 180
taccagcaga agccaggatc ctcccccaaa ccctggattt atgccccatc caacctggct 240
tctggagtcc ctgctcgctt cagtggcagt gggctctggga cctcttactc tctcacaatc 300
agcagagtgg aggtgaaga tgctgccact tattactgcc agcagtggag ttttaaccca 360
cccacgttcg gtgctgggac caagctggag ctgaaagggt gcggtggctc gggcggtggt 420
ggatctggag gaggtgggag ctctcaggct tatctacagc agtctggggc tgagctgggt 480
aggcctgggg cctcagtga gattgtcctgc aaggcttctg gctacacatt taccagttac 540
aatatgcact gggtaaagca gacacctaga cagggccttg aatggatttg agctatttat 600
ccaggaaatg gtgatacttc ctacaatcag aagttcaagg gcaaggccac actgactgta 660
gacaaatcct ccagcacagc ctacatgcag ctacagagcc tgacatctga agactctgct 720
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gatataatgt taaacaaaga ggagacgaag aaagaaaaca gctttgaaat gcaaaaagggt 1020
gatcagaatc ctcaaattgc ggcacatgtc ataagtgagg ccagcagtaa aacacatctt 1080
gtgtttacagt gggctgaaaa aggatactac accatgagca acaacttggg aacctggaa 1140
aatgggaaac agctgaccgt taaaagacaa ggactctatt atatctatgt ccaagtcacc 1200
ttctgttcca atcgggaagc ttcgagtcaa gctcatttta tagccagcct ctgcctaaag 1260
tcccccggtg gattcgagag aatcttactc agagctgcaa ataccacag ttccgccaaa 1320
ccttgcgggc aacaatccat tcacttggga ggagtatttg aattgcaacc aggtgcttcg 1380
gtgtttgtca atgtgactga tccaagccaa gtgagccatg gcactggctt cacgtccttt 1440
ggcttactca aactcgagtg ataactctaga                                     1470
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<210> 150

<211> 482

<212> PRT

<213> Artificial Sequence

<220>

<223> Mouse-Human hybrid fusion protein

<400> 150

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Val Ile Ile Ala Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile
20      25      30
Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser
35      40      45
Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser
50      55      60
Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro
65      70      75      80
Ala Arg Phe Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
85      90      95
Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
100     105     110
Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
115     120     125
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Ser
130     135     140
Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala
145     150     155     160
Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
165     170     175
Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile
180     185     190
Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
195     200     205
Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Thr Ala Tyr
210     215     220
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
225     230     235     240
Ala Arg Val Val Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp
245     250     255
Gly Thr Gly Thr Thr Val Thr Val Ser Asp Pro Arg Arg Leu Asp Lys
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Ile	Glu	Asp	Glu	Arg	Asn	Leu	His	Glu	Asp	Phe	Val	Phe	Met	Lys	Thr
		275					280					285			
Ile	Gln	Arg	Cys	Asn	Thr	Gly	Glu	Arg	Ser	Leu	Ser	Leu	Leu	Asn	Cys
	290					295					300				
Glu	Glu	Ile	Lys	Ser	Gln	Phe	Glu	Gly	Phe	Val	Lys	Asp	Ile	Met	Leu
305					310					315					320
Asn	Lys	Glu	Glu	Thr	Lys	Lys	Glu	Asn	Ser	Phe	Glu	Met	Gln	Lys	Gly
				325					330					335	
Asp	Gln	Asn	Pro	Gln	Ile	Ala	Ala	His	Val	Ile	Ser	Glu	Ala	Ser	Ser
			340					345					350		
Lys	Thr	Thr	Ser	Val	Leu	Gln	Trp	Ala	Glu	Lys	Gly	Tyr	Tyr	Thr	Met
		355					360					365			
Ser	Asn	Asn	Leu	Val	Thr	Leu	Glu	Asn	Gly	Lys	Gln	Leu	Thr	Val	Lys
	370					375					380				
Arg	Gln	Gly	Leu	Tyr	Tyr	Ile	Tyr	Ala	Gln	Val	Thr	Phe	Cys	Ser	Asn
385					390					395					400
Arg	Glu	Ala	Ser	Ser	Gln	Ala	Pro	Phe	Ile	Ala	Ser	Leu	Cys	Leu	Lys
				405					410					415	
Ser	Pro	Gly	Arg	Phe	Glu	Arg	Ile	Leu	Leu	Arg	Ala	Ala	Asn	Thr	His
			420					425					430		
Ser	Ser	Ala	Lys	Pro	Cys	Gly	Gln	Gln	Ser	Ile	His	Leu	Gly	Gly	Val
		435					440					445			
Phe	Glu	Leu	Gln	Pro	Gly	Ala	Ser	Val	Phe	Val	Asn	Val	Thr	Asp	Pro
	450					455					460				
Ser	Gln	Val	Ser	His	Gly	Thr	Gly	Phe	Thr	Ser	Phe	Gly	Leu	Leu	Lys
465					470					475					480
Leu	Glu														

<210> 151
<211> 1290
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse-Human hybrid fusion protein

<400> 151

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ccaggggaga	aggtcacaat	gacttgcagg	gccagctcaa	gtgtaagtta	catgcactgg	180
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tctggagtc	ctgctcgctt	cagtggcagt	gggtctggga	ctcttactc	tctcacaatc	300
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cccacgttcg	gtgctgggac	caagctggag	ctgaaagggt	gcgggtggctc	gggcgggtggt	420
ggatctggag	gaggtgggag	ctctcaggct	tatctacagc	agictggggc	tgagctgggtg	480
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ccaggaaaatg	gtgatacttc	ctacaatcag	aagttcaagg	gcaaggccac	actgactgta	660
gacaaatcct	ccagcacagc	ctacatgcag	ctcagcagcc	tgacatctga	agactctgcg	720
gtctatttct	gtgcaagagt	ggtgtactat	agtaactctt	actgggtactt	cgatgtctgg	780
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aatgggaaac	agctgaccgt	taaaagacaa	ggactctatt	atatctatgc	ccaagtcacc	1020
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tcccccggtg	gatttcgagag	aatcttactc	agagctgcaa	atacccacag	ttccgcca	1140
ccttgcgggc	aacaatccat	tcacttggga	ggagtatttg	aattgcaacc	aggtgcttcg	1200
gtgtttgtca	atgtgactga	tccaagccaa	gtgagccatg	gcactggcctt	cactgccttt	1260
ggcttactca	aactcgagtg	ataatctaga				1290

<210> 152
<211> 422
<212> PRT
<213> Artificial Sequence

<220>

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
<223> Mouse-Human hybrid fusion protein

<400> 152

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Val Ile Ile Ala Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile
 20      25      30
Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser
 35      40      45
Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser
 50      55      60
Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro
 65      70      75      80
Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
 85      90      95
Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
100      105      110
Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
115      120      125
Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Ser
130      135      140
Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala
145      150      155      160
Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
165      170      175
Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile
180      185      190
Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
195      200      205
Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Thr Ala Tyr
210      215      220
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
225      230      235      240
Ala Arg Val Val Tyr Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp
245      250      255
Gly Thr Gly Thr Thr Val Thr Val Ser Asp Pro Glu Asn Ser Phe Glu
260      265      270
Met Gln Lys Gly Asp Gln Asn Pro Gln Ile Ala Ala His Val Ile Ser
275      280      285
Glu Ala Ser Ser Lys Thr Thr Ser Val Leu Gln Trp Ala Glu Lys Gly
290      295      300
Tyr Tyr Thr Met Ser Asn Asn Leu Val Thr Leu Glu Asn Gly Lys Gln
305      310      315      320
Leu Thr Val Lys Arg Gln Gly Leu Tyr Tyr Ile Tyr Ala Gln Val Thr
325      330      335
Phe Cys Ser Asn Arg Glu Ala Ser Ser Gln Ala Pro Phe Ile Ala Ser
340      345      350
Leu Cys Leu Lys Ser Pro Gly Arg Phe Glu Arg Ile Leu Arg Ala
355      360      365
Ala Asn Thr His Ser Ser Ala Lys Pro Cys Gly Gln Gln Ser Ile His
370      375      380
Leu Gly Gly Val Phe Glu Leu Gln Pro Gly Ala Ser Val Phe Val Asn
385      390      395      400
Val Thr Asp Pro Ser Gln Val Ser His Gly Thr Gly Phe Thr Ser Phe
405      410      415
Gly Leu Leu Lys Leu Glu
420

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<210> 153

<211> 3630

<212> DNA

<213> Homo sapiens

<400> 153

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cgcgcggtg agaaccgccg ggaccgcacg tgggcgccgc gcgcttcccc cgcttcccag 180
gtgggcgccg gccgccaggc cacctcacgt ccggcccccg ggatgcgcgt cctcctcgcc 240

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gagttggagg	aggagctgga	ggcggaccat	acccccact	accccgagca	ggagacagaa	1920
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Ser Val Tyr Cys Asn Gly Ser Gln Ile Thr Gly Ser Ser Asn Ile Thr
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Val Tyr Gly Leu Pro Glu Arg Val Glu Leu Ala Pro Leu Pro Pro Trp
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 225 230 235 240
 Cys Thr Leu Asp Gly Leu Phe Pro Ala Ser Glu Ala Gln Val Tyr Leu
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Gly Asn Gly Met Val Ser Arg Cys Ser Arg Ser Gln Asn Thr Val Cys
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Arg Pro Cys Gly Pro Gly Phe Tyr Asn Asp Val Val Ser Ser Lys Pro
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85 90 95
Gln Leu Cys Thr Ala Thr Gln Asp Thr Val Cys Arg Cys Arg Ala Gly
100 105 110
Thr Gln Pro Leu Asp Ser Tyr Lys Pro Gly Val Asp Cys Ala Pro Cys
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Pro Pro Gly His Phe Ser Pro Gly Asp Asn Gln Ala Cys Lys Pro Trp
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Ser Ser Asp Ala Ile Cys Glu Asp Arg Asp Pro Pro Ala Thr Gln Pro
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Gln Glu Thr Gln Gly Pro Pro Ala Arg Pro Ile Thr Val Gln Pro Thr
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Glu Ala Trp Pro Arg Thr Ser Gln Gly Pro Ser Thr Arg Pro Val Glu
195 200 205
Val Pro Gly Gly Arg Ala Val Ala Ala Ile Leu Gly Leu Gly Leu Val
210 215 220
Leu Gly Leu Leu Gly Pro Leu Ala Ile Leu Leu Ala Leu Tyr Leu Leu
225 230 235 240
Arg Arg Asp Gln Arg Leu Pro Pro Asp Ala His Lys Pro Pro Gly Gly
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 Ala Gly Cys Ser Met Cys Glu Gln Asp Cys Lys Gln Gly Gln Glu Leu
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 130 135 140
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 165 170 175
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 180 185 190
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 Arg Phe Ser Val Val Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe
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<400> 162

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Lys	Phe	Cys	His	Ser	Gln	Leu	Ser	Asn	Asn	Ser	Val	Ser	Phe	Phe	Leu
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Tyr	Asn	Leu	Asp	His	Ser	His	Ala	Asn	Tyr	Tyr	Phe	Cys	Asn	Leu	Ser
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<213> Homo sapiens

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 35 40 45
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 65 70 75 80
 Pro Arg Gly Met Tyr Gln Cys Lys Gly Ser Gln Asn Lys Ser Lys Pro
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 <213> Homo sapiens

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt

<210> 166
<211> 207
<212> PRT
<213> Homo sapiens

<400> 166
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Gln Thr Pro Tyr Lys Val Ser Ile Ser Gly Thr Thr Val Ile Leu Thr
35 40 45
Cys Pro Gln Tyr Pro Gly Ser Glu Ile Leu Trp Gln His Asn Asp Lys
50 55 60
Asn Ile Gly Gly Asp Glu Asp Asp Lys Asn Ile Gly Ser Asp Glu Asp
65 70 75 80
His Leu Ser Leu Lys Glu Phe Ser Glu Leu Glu Gln Ser Gly Tyr Tyr
85 90 95
Val Cys Tyr Pro Arg Gly Ser Lys Pro Glu Asp Ala Asn Phe Tyr Leu
100 105 110
Tyr Leu Arg Ala Arg Val Cys Glu Asn Cys Met Glu Met Asp Val Met
115 120 125
Ser Val Ala Thr Ile Val Ile Val Asp Ile Cys Ile Thr Gly Gly Leu
130 135 140
Leu Leu Leu Val Tyr Tyr Trp Ser Lys Asn Arg Lys Ala Lys Ala Lys
145 150 155 160
Pro Val Thr Arg Gly Ala Gly Ala Gly Gly Arg Gln Arg Gly Gln Asn
165 170 175
Lys Glu Arg Pro Pro Pro Val Pro Asn Pro Asp Tyr Glu Pro Ile Arg
180 185 190
Lys Gly Gln Arg Asp Leu Tyr Ser Gly Leu Asn Gln Arg Arg Ile
195 200 205

<210> 167
<211> 3
<212> DNA
<213> Homo sapiens - to be filled in

<220>
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<222> 1, 2, 3
<223> n = A,T,C or G

<400> 167
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3

<210> 168
<211> 2
<212> PRT
<213> Homo sapiens - to be filled in

<220>
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<222> 1, 2
<223> Xaa = Any Amino Acid

<400> 168
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<210> 169
<211> 3084
<212> DNA
<213> Homo sapiens

<400> 169
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<210> 170
 <211> 458
 <212> PRT
 <213> Homo sapiens

<400> 170
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 35 40 45
 Ile Gln Phe His Trp Lys Asn Ser Asn Gln Ile Lys Ile Leu Gly Asn
 50 55 60
 Gln Gly Ser Phe Leu Thr Lys Gly Pro Ser Lys Leu Asn Asp Arg Ala
 65 70 75 80
 Asp Ser Arg Arg Ser Leu Trp Asp Gln Gly Asn Phe Pro Leu Ile Ile

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Ser	Asp	Thr	His	Leu	Leu	Gln	Gly	Gln	Ser	Leu	Thr	Leu	Thr	Leu	Glu
Ser	Pro	Pro	Gly	Ser	Ser	Pro	Ser	Val	Gln	Cys	Arg	Ser	Pro	Arg	Gly
Lys	Asn	Ile	Gln	Gly	Gly	Lys	Thr	Leu	Ser	Val	Ser	Gln	Leu	Glu	Leu
Gln	Asp	Ser	Gly	Thr	Trp	Thr	Cys	Thr	Val	Leu	Gln	Asn	Gln	Lys	Lys
Val	Glu	Phe	Lys	Ile	Asp	Ile	Val	Val	Leu	Ala	Phe	Gln	Lys	Ala	Ser
Ser	Ile	Val	Tyr	Lys	Lys	Glu	Gly	Glu	Gln	Val	Glu	Phe	Ser	Phe	Pro
Leu	Ala	Phe	Thr	Val	Glu	Lys	Leu	Thr	Gly	Ser	Gly	Glu	Leu	Trp	Trp
Gln	Ala	Glu	Arg	Ala	Ser	Ser	Ser	Lys	Ser	Trp	Ile	Thr	Phe	Asp	Leu
Lys	Asn	Lys	Glu	Val	Ser	Val	Lys	Arg	Val	Thr	Gln	Asp	Pro	Lys	Leu
Gln	Met	Gly	Lys	Lys	Leu	Pro	Leu	His	Leu	Thr	Leu	Pro	Gln	Ala	Leu
Pro	Gln	Tyr	Ala	Gly	Ser	Gly	Asn	Leu	Thr	Leu	Ala	Leu	Glu	Ala	Lys
Thr	Gly	Lys	Leu	His	Gln	Glu	Val	Asn	Leu	Val	Val	Met	Arg	Ala	Thr
Gln	Leu	Gln	Lys	Asn	Leu	Thr	Cys	Glu	Val	Trp	Gly	Pro	Thr	Ser	Pro
Lys	Leu	Met	Leu	Ser	Leu	Lys	Leu	Glu	Asn	Lys	Glu	Ala	Lys	Val	Ser
Lys	Arg	Glu	Lys	Ala	Val	Trp	Val	Leu	Asn	Pro	Glu	Ala	Gly	Met	Trp
Gln	Cys	Leu	Leu	Ser	Asp	Ser	Gly	Gln	Val	Leu	Leu	Glu	Ser	Asn	Ile
Lys	Val	Leu	Pro	Thr	Trp	Ser	Thr	Pro	Val	Gln	Pro	Met	Ala	Leu	Ile
Val	Leu	Gly	Gly	Val	Ala	Gly	Leu	Leu	Leu	Phe	Ile	Gly	Leu	Gly	Ile
Phe	Phe	Cys	Val	Arg	Cys	Arg	His	Arg	Arg	Arg	Gln	Ala	Glu	Arg	Met
Ser	Gln	Ile	Lys	Arg	Leu	Leu	Ser	Glu	Lys	Lys	Thr	Cys	Gln	Cys	Pro
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<210> 171
<211> 2308
<212> DNA
<213> Homo sapiens

<400> 171

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atggagacca	gtcagtttcc	aggtgaagag	aagcctcagg	caagccccga	aggccgtcct	780
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<210> 172
 <211> 272
 <212> PRT
 <213> Homo sapiens

<400> 172

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His	Ala	Thr	Phe	Lys	Ala	Met	Ala	Tyr	Lys	Glu	Gly	Thr	Met	Leu	Asn
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Cys	Glu	Cys	Lys	Arg	Gly	Phe	Arg	Arg	Ile	Lys	Ser	Gly	Ser	Leu	Tyr
	50					55					60				
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Gln	Pro	Glu	Glu	Gln	Lys	Glu	Arg	Lys	Thr	Thr	Glu	Met	Gln	Ser	Pro
				100				105						110	
Met	Gln	Pro	Val	Asp	Gln	Ala	Ser	Leu	Pro	Gly	His	Cys	Arg	Glu	Pro
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		130				135					140				
Gly	Gln	Met	Val	Tyr	Tyr	Gln	Cys	Val	Gln	Gly	Tyr	Arg	Ala	Leu	His
	145				150					155				160	
Arg	Gly	Pro	Ala	Glu	Ser	Val	Cys	Lys	Met	Thr	His	Gly	Lys	Thr	Arg
				165					170					175	
Trp	Thr	Gln	Pro	Gln	Leu	Ile	Cys	Thr	Gly	Glu	Met	Glu	Thr	Ser	Gln
		180						185						190	
Phe	Pro	Gly	Glu	Glu	Lys	Pro	Gln	Ala	Ser	Pro	Glu	Gly	Arg	Pro	Glu
		195				200						205			
Ser	Glu	Thr	Ser	Cys	Leu	Val	Thr	Thr	Thr	Asp	Phe	Gln	Ile	Gln	Thr
	210					215					220				
Glu	Met	Ala	Ala	Thr	Met	Glu	Thr	Ser	Ile	Phe	Thr	Thr	Glu	Tyr	Gln
	225				230					235				240	
Val	Ala	Val	Ala	Gly	Cys	Val	Phe	Leu	Leu	Ile	Ser	Val	Leu	Leu	Leu
				245				250						255	
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<210> 173

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<211> 1060

<212> DNA

<213> Homo sapiens

<400> 173

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<210> 174

<211> 235

<212> PRT

<213> Homo sapiens

<400> 174

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Trp Asn Leu Gly Glu Thr Val Glu Leu Lys Cys Gln Val Leu Leu Ser
35     40     45
Asn Pro Thr Ser Gly Cys Ser Trp Leu Phe Gln Pro Arg Gly Ala Ala
50     55     60
Ala Ser Pro Thr Phe Leu Leu Tyr Leu Ser Gln Asn Lys Pro Lys Ala
65     70     75     80
Ala Glu Gly Leu Asp Thr Gln Arg Phe Ser Gly Lys Arg Leu Gly Asp
85     90     95
Thr Phe Val Leu Thr Leu Ser Asp Phe Arg Arg Glu Asn Glu Gly Tyr
100    105    110
Tyr Phe Cys Ser Ala Leu Ser Asn Ser Ile Met Tyr Phe Ser His Phe
115    120    125
Val Pro Val Phe Leu Pro Ala Lys Pro Thr Thr Thr Pro Ala Pro Arg
130    135    140
Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg
145    150    155    160
Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly
165    170    175
Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr
180    185    190
Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Asn His
195    200    205
Arg Asn Arg Arg Arg Val Cys Lys Cys Pro Arg Pro Val Val Lys Ser
210    215    220
Gly Asp Lys Pro Ser Leu Ser Ala Arg Tyr Val
225    230    235

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<210> 175

<211> 4740

<212> DNA

<213> Homo sapiens

<400> 175

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<400> 176
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 Gly Phe Gly Gln Ser Val Val Gln Leu Gln Gly Ser Arg Val Val Val
 35 40 45
 Gly Ala Pro Gln Glu Ile Val Ala Ala Asn Gln Arg Gly Ser Leu Tyr
 50 55 60
 Gln Cys Asp Tyr Ser Thr Gly Ser Cys Glu Pro Ile Arg Leu Gln Val
 65 70 75 80
 Pro Val Glu Ala Val Asn Met Ser Leu Gly Leu Ser Leu Ala Ala Thr
 85 90 95
 Thr Ser Pro Pro Gln Leu Leu Ala Cys Gly Pro Thr Val His Gln Thr
 100 105 110
 Cys Ser Glu Asn Thr Tyr Val Lys Gly Leu Cys Phe Leu Phe Gly Ser
 115 120 125
 Asn Leu Arg Gln Gln Pro Gln Lys Phe Pro Glu Ala Leu Arg Gly Cys
 130 135 140
 Pro Gln Glu Asp Ser Asp Ile Ala Phe Leu Ile Asp Gly Ser Gly Ser
 145 150 155 160
 Ile Ile Pro His Asp Phe Arg Arg Met Lys Glu Phe Val Ser Thr Val
 165 170 175
 Met Glu Gln Leu Lys Ser Lys Thr Leu Phe Ser Leu Met Gln Tyr
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 Ser Glu Glu Phe Arg Ile His Phe Thr Phe Lys Glu Phe Gln Asn Asn
 195 200 205
 Pro Asn Pro Arg Ser Leu Val Lys Pro Ile Thr Gln Leu Gly Arg
 210 215 220
 Thr His Thr Ala Thr Gly Ile Arg Lys Val Val Arg Glu Leu Phe Asn
 225 230 235 240
 Ile Thr Asn Gly Ala Arg Lys Asn Ala Phe Lys Ile Leu Val Val Ile
 245 250 255
 Thr Asp Gly Glu Lys Phe Gly Asp Pro Leu Gly Tyr Glu Asp Val Ile
 260 265 270
 Pro Glu Ala Asp Arg Glu Gly Val Ile Arg Tyr Val Ile Gly Val Gly
 275 280 285
 Asp Ala Phe Arg Ser Glu Lys Ser Arg Gln Glu Leu Asn Thr Ile Ala
 290 295 300
 Ser Lys Pro Pro Arg Asp His Val Phe Gln Val Asn Asn Phe Glu Ala
 305 310 315 320
 Leu Lys Thr Ile Gln Asn Gln Leu Arg Glu Lys Ile Phe Ala Ile Glu
 325 330 335
 Gly Thr Gln Thr Gly Ser Ser Ser Ser Phe Glu His Glu Met Ser Gln
 340 345 350
 Glu Gly Phe Ser Ala Ala Ile Thr Ser Asn Gly Pro Leu Leu Ser Thr
 355 360 365
 Val Gly Ser Tyr Asp Trp Ala Gly Gly Val Phe Leu Tyr Thr Ser Lys
 370 375 380
 Glu Lys Ser Thr Phe Ile Asn Met Thr Arg Val Asp Ser Asp Met Asn
 385 390 395 400
 Asp Ala Tyr Leu Gly Tyr Ala Ala Ala Ile Ile Leu Arg Asn Arg Val
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 Lys Gly Thr Gln Ile Gly Ala Tyr Phe Gly Ala Ser Leu Cys Ser Val
 450 455 460
 Asp Val Asp Ser Asn Gly Ser Thr Asp Leu Val Leu Ile Gly Ala Pro
 465 470 475 480
 His Tyr Tyr Glu Gln Thr Arg Gly Gly Gln Val Ser Val Cys Pro Leu
 485 490 495
 Pro Arg Gly Gln Arg Ala Arg Trp Gln Cys Asp Ala Val Leu Tyr Gly
 500 505 510
 Glu Gln Gly Gln Pro Trp Gly Arg Phe Gly Ala Ala Leu Thr Val Leu
 515 520 525
 Gly Asp Val Asn Gly Asp Lys Leu Thr Asp Val Ala Ile Gly Ala Pro
 530 535 540
 Gly Glu Glu Asp Asn Arg Gly Ala Val Tyr Leu Phe His Gly Thr Ser
 545 550 555 560
 Gly Ser Gly Ile Ser Pro Ser His Ser Gln Arg Ile Ala Gly Ser Lys
 565 570 575
 Leu Ser Pro Arg Leu Gln Tyr Phe Gly Gln Ser Leu Ser Gly Gly Gln
 580 585 590
 Asp Leu Thr Met Asp Gly Leu Val Asp Leu Thr Val Gly Ala Gln Gly
 595 600 605
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 Met Glu Phe Asn Pro Arg Glu Val Ala Arg Asn Val Phe Glu Cys Asn
 625 630 635 640
 Asp Gln Val Val Lys Gly Lys Glu Ala Gly Glu Val Arg Val Cys Leu
 645 650 655
 His Val Gln Lys Ser Thr Arg Asp Arg Leu Arg Glu Gly Gln Ile Gln
 660 665 670
 Ser Val Val Thr Tyr Asp Leu Ala Leu Asp Ser Gly Arg Pro His Ser
 675 680 685
 Arg Ala Val Phe Asn Glu Thr Lys Asn Ser Thr Arg Arg Gln Thr Gln
 690 695 700
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 725 730 735
 Ser Leu Val Gly Thr Pro Leu Ser Ala Phe Gly Asn Leu Arg Pro Val
 740 745 750
 Leu Ala Glu Asp Ala Gln Arg Leu Phe Thr Ala Leu Phe Pro Phe Glu
 755 760 765
 Lys Asn Cys Gly Asn Asp Asn Ile Cys Gln Asp Asp Leu Ser Ile Thr
 770 775 780
 Phe Ser Phe Met Ser Leu Asp Cys Leu Val Val Gly Gly Pro Arg Glu
 785 790 795 800
 Phe Asn Val Thr Val Thr Val Arg Asn Asp Gly Glu Asp Ser Tyr Arg
 805 810 815
 Thr Gln Val Thr Phe Phe Phe Pro Leu Asp Leu Ser Tyr Arg Lys Val
 820 825 830
 Ser Thr Leu Gln Asn Gln Arg Ser Gln Arg Ser Trp Arg Leu Ala Cys
 835 840 845
 Glu Ser Ala Ser Ser Thr Glu Val Ser Gly Ala Leu Lys Ser Thr Ser
 850 855 860
 Cys Ser Ile Asn His Pro Ile Phe Pro Glu Asn Ser Glu Val Thr Phe
 865 870 875 880
 Asn Ile Thr Phe Asp Val Asp Ser Lys Ala Ser Leu Gly Asn Lys Leu
 885 890 895
 Leu Leu Lys Ala Asn Val Thr Ser Glu Asn Asn Met Pro Arg Thr Asn
 900 905 910
 Lys Thr Glu Phe Gln Leu Glu Leu Pro Val Lys Tyr Ala Val Tyr Met
 915 920 925
 Val Val Thr Ser His Gly Val Ser Thr Lys Tyr Leu Asn Phe Thr Ala
 930 935 940
 Ser Glu Asn Thr Ser Arg Val Met Gln His Gln Tyr Gln Val Ser Asn
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			980					985					990		
Ser	Asp	Phe	Leu	Ala	Glu	Leu	Arg	Lys	Ala	Pro	Val	Val	Asn	Cys	Ser
			995					1000					1005		
Ile	Ala	Val	Cys	Gln	Arg	Ile	Gln	Cys	Asp	Ile	Pro	Phe	Phe	Gly	Ile
			1010					1015					1020		
Gln	Glu	Glu	Phe	Asn	Ala	Thr	Leu	Lys	Gly	Asn	Leu	Ser	Phe	Asp	Trp
			1025					1030					1035		1040
Tyr	Ile	Lys	Thr	Ser	His	Asn	His	Leu	Leu	Ile	Val	Ser	Thr	Ala	Glu
			1045					1050					1055		
Ile	Leu	Phe	Asn	Asp	Ser	Val	Phe	Thr	Leu	Leu	Pro	Gly	Gln	Gly	Ala
			1060					1065					1070		
Phe	Val	Arg	Ser	Gln	Thr	Glu	Thr	Lys	Val	Glu	Pro	Phe	Glu	Val	Pro
			1075					1080					1085		
Asn	Pro	Leu	Pro	Leu	Ile	Val	Gly	Ser	Ser	Val	Gly	Gly	Leu	Leu	Leu
			1090					1095					1100		
Leu	Ala	Leu	Ile	Thr	Ala	Ala	Leu	Tyr	Lys	Leu	Gly	Phe	Phe	Lys	Arg
			1105					1110					1115		1120
Gln	Tyr	Lys	Asp	Met	Met	Ser	Glu	Gly	Gly	Pro	Pro	Gly	Ala	Glu	Pro
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<211> 1364

<212> DNA

<213> Homo sapiens

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<211> 375

<212> PRT

<213> Homo sapiens

<400> 178

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85 90 95
Gly Ala Ala Gln Val Pro Ala Gln Leu Val Gly Ala Leu Arg Val
100 105 110
Leu Ala Tyr Ser Arg Leu Lys Glu Leu Thr Leu Glu Asp Leu Lys Ile
115 120 125
Thr Gly Thr Met Pro Pro Leu Pro Leu Glu Ala Thr Gly Leu Ala Leu
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145 150 155 160
Leu Ala Glu Leu Gln Trp Leu Lys Pro Gly Leu Lys Val Leu Ser
165 170 175
Ile Ala Gln Ala His Ser Pro Ala Phe Ser Cys Glu Gln Val Arg Ala
180 185 190
Phe Pro Ala Leu Thr Ser Leu Asp Leu Ser Asp Asn Pro Gly Leu Gly
195 200 205
Glu Arg Gly Leu Met Ala Ala Leu Cys Pro His Lys Phe Pro Ala Ile
210 215 220
Gln Asn Leu Ala Leu Arg Asn Thr Gly Met Glu Thr Pro Thr Gly Val
225 230 235 240
Cys Ala Ala Leu Ala Ala Ala Gly Val Gln Pro His Ser Leu Asp Leu
245 250 255
Ser His Asn Ser Leu Arg Ala Thr Val Asn Pro Ser Ala Pro Arg Cys
260 265 270
Met Trp Ser Ser Ala Leu Asn Ser Leu Asn Leu Ser Phe Ala Gly Leu
275 280 285
Glu Gln Val Pro Lys Gly Leu Pro Ala Lys Leu Arg Val Leu Asp Leu
290 295 300
Ser Cys Asn Arg Leu Asn Arg Ala Pro Gln Pro Asp Glu Leu Pro Glu
305 310 315 320
Val Asp Asn Leu Thr Leu Asp Gly Asn Pro Phe Leu Val Pro Gly Thr
325 330 335
Ala Leu Pro His Glu Gly Ser Met Asn Ser Gly Val Val Pro Ala Cys
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355 360 365
Gln Gly Ala Arg Gly Phe Ala
370 375

<210> 179

<211> 2633

<212> DNA

<213> Homo sapiens

<400> 179

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atttgccat	cccagtg cca	cgatctcatg	gtttcgggat	ggccagctgc	tgccaagctc	1380
caattacagc	aatatca aga	tctacaacac	cccctctgcc	agctatctgg	aggtgacccc	1440
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gtccttcgaa	ttcatccttg	ttcaagcaga	cacccccctc	tcaccatcca	tcgaccaggt	1560
ggagccatac	tccagca cag	cccaggtgca	gtttgatgaa	ccagaggcca	caggtggggg	1620
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gtggtatgat	gccaagg aag	ccagcatgga	gggcatcgtc	accatcgtgg	gcctgaagcc	1740
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cgcggcctcc	gagttca aga	cgcagccagt	ccaaggggaa	cccagtgcac	ctaagctcga	1860
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cggctcccc	atcagac act	atctggctag	gtaccgagcg	ctctcctccg	agtggaaacc	1980
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tgtgttcagg	acctcgg ccc	agcccacagc	catcccagcc	aacggcagcc	ccacctcagg	2160
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cctgtgtgga	aaagccggc	cgggggcaa	gggcaaggac	atggaggagg	gcaaggccgc	2340
cttctcga	gatgagt cca	aggagcccat	cgtggaggtt	cgaacggagg	aggagaggac	2400
cccaaacat	gatggaggga	aacacacaga	gcccacagag	accacgccac	tgacggagcc	2460
cgagaagggc	cccgtagaag	caaagccaga	gtgccaggag	acagaaacga	agccagcgcc	2520
agccgaagtc	aagacgg tcc	ccaatgacgc	cacacagaca	aaggagaacg	agagcaaagc	2580
atgatgggtg	aagagaa ccc	agcaaagatc	aaaataaaaa	gtgacacagc	agc	2633

<210> 180
<211> 848
<212> PRT
<213> Homo sapiens

<400> 180

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			20					25					30		
Val	Gly	Glu	Ser	Lys	Phe	Phe	Leu	Cys	Gln	Val	Ala	Gly	Asp	Ala	Lys
		35					40					45			
Asp	Lys	Asp	Ile	Ser	Trp	Phe	Ser	Pro	Asn	Gly	Glu	Lys	Leu	Thr	Pro
	50					55					60				
Asn	Gln	Gln	Arg	Ile	Ser	Val	Val	Trp	Asn	Asp	Asp	Ser	Ser	Ser	Thr
65				70					75					80	
Leu	Thr	Ile	Tyr	Asn	Ala	Asn	Ile	Asp	Asp	Ala	Gly	Ile	Tyr	Lys	Cys
			85					90					95		
Val	Val	Thr	Gly	Glu	Asp	Gly	Ser	Glu	Ser	Glu	Ala	Thr	Val	Asn	Val
		100					105					110			
Lys	Ile	Phe	Gln	Lys	Leu	Met	Phe	Lys	Asn	Ala	Pro	Thr	Pro	Gln	Glu
		115					120				125				
Phe	Arg	Glu	Gly	Glu	Asp	Ala	Val	Ile	Val	Cys	Asp	Val	Val	Ser	Ser
	130					135					140				
Leu	Pro	Pro	Thr	Ile	Ile	Trp	Lys	His	Lys	Gly	Arg	Asp	Val	Ile	Leu
145				150					155					160	
Lys	Lys	Asp	Val	Arg	Phe	Ile	Val	Leu	Ser	Asn	Asn	Tyr	Leu	Gln	Ile
				165				170					175		
Arg	Gly	Ile	Lys	Lys	Thr	Asp	Glu	Gly	Thr	Tyr	Arg	Cys	Glu	Gly	Arg
		180					185						190		
Ile	Leu	Ala	Arg	Gly	Glu	Ile	Asn	Phe	Lys	Asp	Ile	Gln	Val	Ile	Val
		195					200					205			
Asn	Val	Pro	Pro	Thr	Ile	Arg	Ala	Arg	Gln	Asn	Ile	Val	Asn	Ala	Thr
210						215					220				
Ala	Asn	Leu	Gly	Gln	Ser	Val	Thr	Leu	Val	Cys	Asp	Ala	Glu	Arg	Phe
225					230					235				240	
Pro	Glu	Pro	Thr	Met	Ser	Trp	Thr	Lys	Asp	Gly	Glu	Gln	Ile	Glu	Gln
				245					250					255	
Glu	Glu	Asp	Asp	Glu	Lys	Tyr	Ile	Phe	Ser	Asp	Asp	Ser	Ser	Gln	Leu
		260						265					270		
Thr	Ile	Lys	Lys	Val	Asp	Lys	Asn	Asp	Glu	Ala	Glu	Tyr	Ile	Cys	Ile
		275					280					285			
Ala	Glu	Asn	Lys	Ala	Gly	Glu	Gln	Asp	Ala	Thr	Ile	His	Leu	Lys	Val

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290 295 300
Phe Ala Lys Pro Lys Ile Thr Tyr Val Glu Asn Gln Thr Ala Met Glu
305 310 315
Leu Glu Glu Gln Val Thr Leu Thr Cys Glu Ala Ser Gly Asp Pro Ile
325 330 335
Pro Ser Ile Thr Trp Arg Thr Ser Thr Arg Asn Ile Ser Ser Glu Glu
340 345 350
Lys Thr Leu Asp Gly His Met Val Val Arg Ser His Ala Arg Val Ser
355 360 365
Ser Leu Thr Leu Lys Ser Ile Gln Tyr Thr Asp Ala Gly Glu Tyr Ile
370 375 380
Cys Thr Ala Ser Asn Thr Ile Gly Gln Asp Ser Gln Ser Met Tyr Leu
385 390 395 400
Glu Val Gln Tyr Ala Pro Lys Leu Gln Gly Pro Val Ala Val Tyr Thr
405 410 415
Trp Glu Gly Asn Gln Val Asn Ile Thr Cys Glu Val Phe Ala Tyr Pro
420 425 430
Ser Ala Thr Ile Ser Trp Phe Arg Asp Gly Gln Leu Leu Pro Ser Ser
435 440 445
Asn Tyr Ser Asn Ile Lys Ile Tyr Asn Thr Pro Ser Ala Ser Tyr Leu
450 455 460
Glu Val Thr Pro Asp Ser Glu Asn Asp Phe Gly Asn Tyr Asn Cys Thr
465 470 475 480
Ala Val Asn Arg Ile Gly Gln Glu Ser Phe Glu Phe Ile Leu Val Gln
485 490 495
Ala Asp Thr Pro Ser Ser Pro Ser Ile Asp Gln Val Glu Pro Tyr Ser
500 505 510
Ser Thr Ala Gln Val Gln Phe Asp Glu Pro Glu Ala Thr Gly Gly Val
515 520 525
Pro Ile Leu Lys Tyr Lys Ala Glu Trp Arg Ala Val Gly Glu Glu Val
530 535 540
Trp His Ser Lys Trp Tyr Asp Ala Lys Glu Ala Ser Met Glu Gly Ile
545 550 555 560
Val Thr Ile Val Gly Leu Lys Pro Glu Thr Thr Tyr Ala Val Arg Leu
565 570 575
Ala Ala Leu Asn Gly Lys Gly Leu Gly Glu Ile Ser Ala Ala Ser Glu
580 585 590
Phe Lys Thr Gln Pro Val Gln Gly Glu Pro Ser Ala Pro Lys Leu Glu
595 600 605
Gly Gln Met Gly Glu Asp Gly Asn Ser Ile Lys Val Asn Leu Ile Lys
610 615 620
Gln Asp Asp Gly Gly Ser Pro Ile Arg His Tyr Leu Val Arg Tyr Arg
625 630 635 640
Ala Leu Ser Ser Glu Trp Lys Pro Glu Ile Arg Leu Pro Ser Gly Ser
645 650 655
Asp His Val Met Leu Lys Ser Leu Asp Trp Asn Ala Glu Tyr Glu Val
660 665 670
Tyr Val Val Ala Glu Asn Gln Gln Gly Lys Ser Lys Ala Ala His Phe
675 680 685
Val Phe Arg Thr Ser Ala Gln Pro Thr Ala Ile Pro Ala Asn Gly Ser
690 695 700
Pro Thr Ser Gly Leu Ser Thr Gly Ala Ile Val Gly Ile Leu Ile Val
705 710 715 720
Ile Phe Val Leu Leu Val Val Val Asp Ile Thr Cys Tyr Phe Leu
725 730 735
Asn Lys Cys Gly Leu Phe Met Cys Ile Ala Val Asn Leu Cys Gly Lys
740 745 750
Ala Gly Pro Gly Ala Lys Gly Lys Asp Met Glu Glu Gly Lys Ala Ala
755 760 765
Phe Ser Lys Asp Glu Ser Lys Glu Pro Ile Val Glu Val Arg Thr Glu
770 775 780
Glu Glu Arg Thr Pro Asn His Asp Gly Gly Lys His Thr Glu Pro Asn
785 790 795 800
Glu Thr Thr Pro Leu Thr Glu Pro Glu Lys Gly Pro Val Glu Ala Lys
805 810 815
Pro Glu Cys Gln Glu Thr Glu Thr Lys Pro Ala Pro Ala Glu Val Lys
820 825 830
Thr Val Pro Asn Asp Ala Thr Gln Thr Lys Glu Asn Glu Ser Lys Ala
835 840 845

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<210> 181
<211> 1702
<212> DNA
<213> Homo sapiens

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<400> 181
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ttgcatccgg agagtggaca agaaaatgat gccaccagtc cccattttctc aacacgtcat 180
gaaggggtcct tccaagttcc tgtcctgtgt gctgtaatga atgtgggtctt catcaccatt 240
ttaatcatag ctctcattgc cttatcagtg ggccaataca attgtccagg ccaatacaca 300
ttctcaatgc catcagacag ccatgtttct tcatgctctg aggactgggt tggctaccag 360
aggaaatgct actttatttc tactgtgaag aggagctgga cttcagccca aaatgcttgt 420
tctgaacatg gtgctactct tgctgtcatt gattctgaaa aggacatgaa ctttctaaaa 480
cgatacgtag gtagagagga acactgggtt ggactgaaaa aggaacctgg tcacccatgg 540
aagtgggtcaa atggcacaaga atttaacaac tggttcaacg ttacagggtc tgacaagtgt 600
gttttttctga aaaacacaga ggtcagcagc atggaatgtg agaagaattt atactggata 660
tgtaacaaac cttacaaata ataaggaaac atgttcactt attgactatt atagaatgga 720
actcaaggaa atctgtgtca gtggatgctg ctctgtggtc cgaagtcttc catagagact 780
ttgtgaaaaa aaattttata gtgtcttggg aattttcttc caaacagaac tatggaaaaa 840
aaggaagaaa ttccaggaaa atctgcactg tgggctttta ttgccatgag ctagaagcat 900
cacagggttga ccaataacca tgcccaagaa tgagaagaat gactatgcaa cctttggatg 960
cacttttatat tattttgaat ccagaaataa tgaaataact aggcgtggac ttactattta 1020
ttgctgaatg actaccaaca gtgagagccc ttcatgcatt tgcactactg gaaggagtta 1080
gatgtttggtg ctgatactg aatgtaaaca aaggaattat ggctggtaac ataggttttt 1140
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taagatttgt aatattttctc tctttttaga gaaatttgcc aattttacttt gttatttttc 1260
cccaaaaaga atgggatgat cgtgtatttta tttttttact tcctcagctg tagacaggtc 1320
cttttcgatg gtacataatt ctttgccttt ataactcttt atacagtgtc ttacagagaa 1380
aagacataag caaagactat gaggaatatt tgcaagacat agaatagtg tggaataatg 1440
gcaatatgtg atgtggcaaa tctctattag gaaatattct gtaatcttca gacctagaat 1500
aatactagtc ttataatagg ttgtgtgactt tcctaaatca attctattac gtgcaatact 1560
tcaatacttc atttaaaata tttttatgtg caataaaatg tatttgtttg tattttgtgt 1620
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aaaaaaaaa aaaaaaaaaa aa 1702
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<210> 182
<211> 199
<212> PRT
<213> Homo sapiens

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<400> 182
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Glu Ser Gly Gln Glu Asn Asp Ala Thr Ser Pro His Phe Ser Thr Arg
20 25 30
His Glu Gly Ser Phe Gln Val Pro Val Leu Cys Ala Val Met Asn Val
35 40 45
Val Phe Ile Thr Ile Leu Ile Ile Ala Leu Ile Ala Leu Ser Val Gly
50 55 60
Gln Tyr Asn Cys Pro Gly Gln Tyr Thr Phe Ser Met Pro Ser Asp Ser
65 70 75 80
His Val Ser Ser Cys Ser Glu Asp Trp Val Gly Tyr Gln Arg Lys Cys
85 90 95
Tyr Phe Ile Ser Thr Val Lys Arg Ser Trp Thr Ser Ala Gln Asn Ala
100 105 110
Cys Ser Glu His Gly Ala Thr Leu Ala Val Ile Asp Ser Glu Lys Asp
115 120 125
Met Asn Phe Leu Lys Arg Tyr Ala Gly Arg Glu Glu His Trp Val Gly
130 135 140
Leu Lys Lys Glu Pro Gly His Pro Trp Lys Trp Ser Asn Gly Lys Glu
145 150 155 160
Phe Asn Asn Trp Phe Asn Val Thr Gly Ser Asp Lys Cys Val Phe Leu
165 170 175
Lys Asn Thr Glu Val Ser Ser Met Glu Cys Glu Lys Asn Leu Tyr Trp
180 185 190
Ile Cys Asn Lys Pro Tyr Lys
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195

<210> 183
<211> 1642
<212> DNA
<213> Homo sapiens

<400> 183
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gaccccgcca tggacccggt cctgggtgctg ctgcactcgg tgtcgtccag cctgtcgcagc 180
agcgagctga ccgagctcaa gttcctatgc ctccgggcgcg tgggcaagcg caagctggag 240
cgcgctgcaga ggggcctaga cctcttctcc atgctgctgg agcagaacga cctggagccc 300
gggcacaccg agctcctgcg cgagctgctc gcctccctgc ggcggccacga cctgctgcgg 360
cgcgctgcagc acttcgagggc gggggcgggcg gccgggggccc cgcctgggga agaagacctg 420
tgtgagcagc ttaacgtcat atgtgataat gtggggaaag attggagaag gctggctcgt 480
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tggaactcag acgcatctac ctccgaagcg tcctgatggg ccgctgcttt gcgctggtgg 780
accacaggca tctacacagc ctggactttg gttctctcca ggaaggtagc ccagcactgt 840
gaagaccag caggaagcca ggctgagtg gccacagacc acctgcttct gaactcaagc 900
tgcgtttatt aatgcctctc ccgcaccagg ccgggcttgg gccctgcaca gatatttcca 960
tttcttcctc actatgacac tgagcaagat ctgtctcca ctaaatgagc tcctgcggga 1020
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gtggcgttct gctgcccctg cagttggcag aaaggatgtt ttgtccatt tccttggagg 1260
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taatatctgt gaggtgctga tgagtgattg acacacagca ctctctaaat cttccttgg 1500
aggattatgg gtccctgcaat tctacagttt cttactgttt tgtatcaaaa tcactatctt 1560
tctgataaca gaattgccaa ggcagcggga tctcgtatct ttaaaaagca gtcctcttat 1620
tcctaaggta atcctattaa aa 1642

<210> 184
<211> 208
<212> PRT
<213> Homo sapiens

<400> 184
Met Asp Pro Phe Leu Val Leu Leu His Ser Val Ser Ser Ser Leu Ser
1 5 10 15
Ser Ser Glu Leu Thr Glu Leu Lys Phe Leu Cys Leu Gly Arg Val Gly
20 25 30
Lys Arg Lys Leu Glu Arg Val Gln Ser Gly Leu Asp Leu Phe Ser Met
35 40 45
Leu Leu Glu Gln Asn Asp Leu Glu Pro Gly His Thr Glu Leu Leu Arg
50 55 60
Glu Leu Leu Ala Ser Leu Arg Arg His Asp Leu Leu Arg Arg Val Asp
65 70 75 80
Asp Phe Glu Ala Gly Ala Ala Ala Gly Ala Ala Pro Gly Glu Glu Asp
85 90 95
Leu Cys Ala Ala Phe Asn Val Ile Cys Asp Asn Val Gly Lys Asp Trp
100 105 110
Arg Arg Leu Ala Arg Gln Leu Lys Val Ser Asp Thr Lys Ile Asp Ser
115 120 125
Ile Glu Asp Arg Tyr Pro Arg Asn Leu Thr Glu Arg Val Arg Glu Ser
130 135 140
Leu Arg Ile Trp Lys Asn Thr Glu Lys Glu Asn Ala Thr Val Ala His
145 150 155 160
Leu Val Gly Ala Leu Arg Ser Cys Gln Met Asn Leu Val Ala Asp Leu
165 170 175
Val Gln Glu Val Gln Gln Ala Arg Asp Leu Gln Asn Arg Ser Gly Ala
180 185 190
Met Ser Pro Met Ser Trp Asn Ser Asp Ala Ser Thr Ser Glu Ala Ser

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195 200 205

<210> 185
<211> 1475
<212> DNA
<213> Homo sapiens

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<400> 185
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ggtgagatgg cagctgggca aaatgggcac gaagagtggg tgggcagcgc atacctgttt 120
gtggagtcct cgctggacaa ggtggtcctg tcggatgcct acgcgcaccc ccagcagaag 180
gtggcagtgt acagggctct gcaggctgcc ttggcagaga gcggcgggag cccggacgtg 240
ctgcagatgc tgaagatcca ccgcagcgac ccgcagctga tcgtgcagct gcgattctgc 300
ggcgggcagc cctgtggccg cttcctccgc gcctaccgcg agggggcgct gcgcgccgcg 360
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cgcgccggcg ccgagcggct ggacgctttg ctggcggacg aggagcgctg tttgagttgc 480
atcctagccc agcagcccga ccggtccgg gatgaagaac tggctgagct ggaggatgctg 540
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cccttgacgc ccccggtgcc ctctctgtcg gaggtgaagc cgcgcgccgc gccgccacct 660
gcccagactt ttctgttcca gggtcagcct gtagtgaatc ggccgctgag cctgaaggac 720
caacagacgt tcgcgcgctc tgtgggtctc aaatggcgca aggtggggcg ctactgcag 780
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gaggacttgc tgggcctgac cgatcccaat ggcggcctgg cctagaccag ggtgagacc 1020
agcttttggg gaacctggat ggccttaggg ttcttctgct ggctattgct gaacctctgt 1080
ccatccacgg gacctgaaa ctccacttgg cctatctgct ggacctgctg gggcagagtt 1140
gattgccttc cccaggagcc agaccactgg ggggtgcatca ttggggattc tgcctcaggt 1200
actttgatag agtggtgggt gggggggacc tgctttggag atcagcctca ctttctccca 1260
tcccagaagc ggggcttaca gccagccctt acagtttcac tcatgaagca ccttgatctt 1320
tgggttcctg gacttcatcc tgggtgctgc agatactgca gtgaagtaaa acaggaatca 1380
atcttgcttg cccccagctc acactcagcg tgggaccccg aatgttaagc aatgataata 1440
aagtataaca cggaaaaaaa aaaaaaaaaa aaaaaa 1475
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<210> 186
<211> 312
<212> PRT
<213> Homo sapiens

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<400> 186
Met Ala Ala Gly Gln Asn Gly His Glu Glu Trp Val Gly Ser Ala Tyr
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Leu Phe Val Glu Ser Ser Leu Asp Lys Val Val Leu Ser Asp Ala Tyr
20 25 30
Ala His Pro Gln Gln Lys Val Ala Val Tyr Arg Ala Leu Gln Ala Ala
35 40 45
Leu Ala Glu Ser Gly Gly Ser Pro Asp Val Leu Gln Met Leu Lys Ile
50 55 60
His Arg Ser Asp Pro Gln Leu Ile Val Gln Leu Arg Phe Cys Gly Arg
65 70 75 80
Gln Pro Cys Gly Arg Phe Leu Arg Ala Tyr Arg Glu Gly Ala Leu Arg
85 90 95
Ala Ala Leu Gln Arg Ser Leu Ala Ala Ala Leu Ala Gln His Ser Val
100 105 110
Pro Leu Gln Leu Glu Leu Arg Ala Gly Ala Glu Arg Leu Asp Ala Leu
115 120 125
Leu Ala Asp Glu Glu Arg Cys Leu Ser Cys Ile Leu Ala Gln Gln Pro
130 135 140
Asp Arg Leu Arg Asp Glu Glu Leu Ala Glu Leu Glu Asp Ala Leu Arg
145 150 155 160
Asn Leu Lys Cys Gly Ser Gly Ala Arg Gly Gly Asp Gly Glu Val Ala
165 170 175
Ser Ala Pro Leu Gln Pro Pro Val Pro Ser Leu Ser Glu Val Lys Pro
180 185 190
Pro Pro Pro Pro Pro Ala Gln Thr Phe Leu Phe Gln Gly Gln Pro
195 200 205
Val Val Asn Arg Pro Leu Ser Leu Lys Asp Gln Gln Thr Phe Ala Arg
210 215 220
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Ser Val Gly Leu Lys Trp Arg Lys Val Gly Arg Ser Leu Gln Arg Gly
225 230 235 240
Cys Arg Ala Leu Arg Asp Pro Ala Leu Asp Ser Leu Ala Tyr Glu Tyr
245 250 255
Glu Arg Glu Gly Leu Tyr Glu Gln Ala Phe Gln Leu Leu Arg Arg Phe
260 265 270
Val Gln Ala Glu Gly Arg Arg Ala Thr Leu Gln Arg Leu Val Glu Ala
275 280 285
Leu Glu Glu Asn Glu Leu Thr Ser Leu Ala Glu Asp Leu Leu Gly Leu
290 295 300
Thr Asp Pro Asn Gly Gly Leu Ala
305 310

<210> 187
<211> 600
<212> DNA
<213> Homo sapiens

<400> 187
atggaagcca gagacaagca ggtactccgc tccctgcgtc tggagctggg tgccgaggtg 60
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attcaagaaa tcaaagctca aaccacaggc ctccggaaga caatgctgtt gctggacatc 180
ctgccttcca ggggcccaca agcttttgac accttcctcg attccctcca ggaatttccc 240
tgggtaagag agaagctgga gaaggcgaga gaggaagtca cagccgagct gcctacaggt 300
gactggatgg ccggaatccc ctacacatc ctacagcagc cgccatcaga ccagcagatt 360
aaccagctgg ctcaagaagt agggcccgag tgggagcccg tggctcctgtc tctgggactg 420
tcccagaccg acatctaccg ctgcaaggcc aaccatcccc acaacgtgca ttcgcaggtg 480
gtggaggcct ttgtccgctg gcgccagcgt ttgggaagc aggccacatt cctaagctta 540
cacaagggcc tccaggcagt ggaggctgat ccctccctgc tccagcacat gctggagtga 600

<210> 188
<211> 199
<212> PRT
<213> Homo sapiens

<400> 188
Met Glu Ala Arg Asp Lys Gln Val Leu Arg Ser Leu Arg Leu Glu Leu
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Gly Ala Glu Val Leu Val Glu Gly Leu Val Leu Gln Tyr Leu Tyr Gln
20 25 30
Glu Gly Ile Leu Thr Glu Asn His Ile Gln Glu Ile Lys Ala Gln Thr
35 40 45
Thr Gly Leu Arg Lys Thr Met Leu Leu Leu Asp Ile Leu Pro Ser Arg
50 55 60
Gly Pro Lys Ala Phe Asp Thr Phe Leu Asp Ser Leu Gln Glu Phe Pro
65 70 75 80
Trp Val Arg Glu Lys Leu Glu Lys Ala Arg Glu Glu Val Thr Ala Glu
85 90 95
Leu Pro Thr Gly Asp Trp Met Ala Gly Ile Pro Ser His Ile Leu Ser
100 105 110
Ser Ser Pro Ser Asp Gln Gln Ile Asn Gln Leu Ala Gln Lys Leu Gly
115 120 125
Pro Glu Trp Glu Pro Val Val Leu Ser Leu Gly Leu Ser Gln Thr Asp
130 135 140
Ile Tyr Arg Cys Lys Ala Asn His Pro His Asn Val His Ser Gln Val
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Val Glu Ala Phe Val Arg Trp Arg Gln Arg Phe Gly Lys Gln Ala Thr
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Leu Leu Gln His Met Leu Glu
195

<210> 189
<211> 1642
<212> DNA

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PCT/US2003/024918

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
<213> Homo sapiens

<400> 189
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<210> 190

<211> 208

<212> PRT

<213> Homo sapiens

<400> 190

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Glu	Leu	Leu	Ala	Ser	Leu	Arg	Arg	His	Asp	Leu	Leu	Arg	Arg	Val	Asp
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Leu	Val	Gly	Ala	Leu	Arg	Ser	Cys	Gln	Met	Asn	Leu	Val	Ala	Asp	Leu
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Val	Gln	Glu	Val	Gln	Gln	Ala	Arg	Asp	Leu	Gln	Asn	Arg	Ser	Gly	Ala
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<210> 191

<211> 3492

<212> DNA

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<213> Homo sapiens

<400> 191

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<210> 192

<211> 425

<212> PRT

<213> Homo sapiens

<400> 192

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 35 40 45
 Gln Leu Trp Asn Trp Val Pro Glu Cys Leu Ser Cys Gly Ser Arg Cys
 50 55 60
 Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg Glu Gln Asn Arg
 65 70 75 80
 Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu Ser Lys Gln Glu
 85 90 95
 Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg Pro Gly Phe Gly
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 Val Ala Arg Pro Gly Thr Glu Thr Ser Asp Val Val Cys Lys Pro Cys
 115 120 125
 Ala Pro Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr Asp Ile Cys Arg
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 Pro His Gln Ile Cys Asn Val Val Ala Ile Pro Gly Asn Ala Ser Met
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 Asp Ala Val Cys Thr Ser Thr Ser Pro Thr Arg Ser Met Ala Pro Gly
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 Ala Val His Leu Pro Gln Pro Val Ser Thr Arg Ser Gln His Thr Gln
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 Pro Thr Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser Phe Leu Leu Pro
 195 200 205
 Met Gly Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly Asp Phe Ala Leu
 210 215 220
 Pro Val Gly Leu Ile Val Gly Val Thr Ala Leu Gly Leu Leu Ile Ile
 225 230 235 240
 Gly Val Val Asn Cys Val Ile Met Thr Gln Val Lys Lys Lys Pro Leu
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 Cys Leu Gln Arg Glu Ala Lys Val Pro His Leu Pro Ala Asp Lys Ala
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 Arg Gly Thr Gln Gly Pro Glu Gln His Leu Leu Ile Thr Ala Pro
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 Arg Ala Pro Thr Arg Asn Gln Pro Gln Ala Pro Gly Val Glu Ala Ser
 305 310 315 320
 Gly Ala Gly Glu Ala Arg Ala Ser Thr Gly Ser Ser Asp Ser Ser Pro
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 Gly Gly His Gly Thr Gln Val Asn Val Thr Cys Ile Val Asn Val Cys
 340 345 350
 Ser Ser Ser Asp His Ser Ser Gln Cys Ser Ser Gln Ala Ser Ser Thr
 355 360 365
 Met Gly Asp Thr Asp Ser Ser Pro Ser Glu Ser Pro Lys Asp Glu Gln
 370 375 380
 Val Pro Phe Ser Lys Glu Glu Cys Ala Phe Arg Ser Gln Leu Glu Thr
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<210> 193
 <211> 1799
 <212> DNA
 <213> Homo sapiens

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<210> 194
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<212> PRT
<213> Homo sapiens

<400> 194

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Cys	Pro	Pro	Gly	His	His	Ile	Ser	Glu	Asp	Gly	Arg	Asp	Cys	Ile	Ser
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	275						280						285		
Glu	Arg	Ser	Gln	Arg	Arg	Arg	Leu	Leu	Val	Pro	Ala	Asn	Glu	Gly	Asp
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 355 360 365
 Ser Val His Thr Leu Leu Asp Ala Leu Glu Thr Leu Gly Glu Arg Leu
 370 375 380
 Ala Lys Gln Lys Ile Glu Asp His Leu Leu Ser Ser Gly Lys Phe Met
 385 390 395 400
 Tyr Leu Glu Gly Asn Ala Asp Ser Ala Leu Ser
 405 410

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 <211> 683
 <212> DNA
 <213> Homo sapiens

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 <212> PRT
 <213> Homo sapiens

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 35 40 45
 Val Leu Leu Ser Val Leu Leu Tyr Gln Trp Ile Leu Cys Gln Gly Ser
 50 55 60
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 65 70 75 80
 Lys Tyr Gly Asn His Cys Tyr Tyr Phe Ser Val Glu Glu Lys Asp Trp
 85 90 95
 Asn Ser Ser Leu Glu Phe Cys Leu Ala Arg Asp Ser His Leu Leu Val
 100 105 110
 Ile Thr Asp Asn Gln Glu Met Ser Leu Leu Gln Val Phe Leu Ser Glu
 115 120 125
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 130 135 140
 Asp Gly Ser Pro Leu Asn Phe Ser Arg Ile Ser Asn Ser Phe Val
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 165 170 175
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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
<213> Homo sapiens

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<213> Homo sapiens

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35 40 45
Ser Ile Met Arg Arg Val Asn His Lys Asp Pro His Val Ala Met Gln
50 55 60
Ala Leu Thr Leu Leu Gly Ala Cys Val Ser Asn Cys Gly Lys Ile Phe

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	Leu	Tyr	Gln	Asn	Ala	Gly	Pro	Asn	Met	Pro	Gln	Val	Pro	Asn	Tyr	Asn	
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Ile	Gln	Asn	Leu	Val	Ser	Ala	Ser	Leu	Gly	Ser	Thr	Ser	Lys	Asn	Thr
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Gln	Ala	Glu	Glu	Met	Ala	Ser	Asp	Asp	Leu	Ser	Leu	Ile	Arg	Lys	Asn
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gaatgggctg agctgcctgt aacttgagag tagatggttt gagcctgagc agagacatga 1860
ctcagcctgt tccatgaagg cagagccatg gaccacgcag gaagggccta cagcccattt 1920
ctccatacgc actggtatgt gtggatgatg ctgccagggc gccatcgcca agtaagaaag 1980
tgaagcaaat cagaaacttg tgaagtggaa atgttctaaa ggtgggtgag caataaaaaa 2040
catagtactc tttgtagcaa aattcttaag taigtatttt tctgttgaag tttacaatca 2100
aaggaaaata gtaatgtttt atactgttta ctgaaagaaa aagacctatg agcacatagg 2160
actctagacg gcatccagcc ggaggccaga gctgagccct cagcccgagg ggcaggctcc 2220
aggcctcagc aggtgcggag ccgtcactgc accaagtctc actggctgtc agtatgacat 2280
ttcacgggag atttcttgtt gctcaaaaaa ttgttcaatg acagtttctt 2340
ttttcttact agacctgtaa cttttgtaaa tacacatagc atgtaatggg atcttaaaag 2400
gtgtttctat gtgacaattt tgtacaaatt tgttattttc catttttatt tcaaaaata 2460
cattcaaact taaaatt 2477
```

<210> 202
<211> 277
<212> PRT
<213> Homo sapiens

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<400> 202
Met Glu Asn Thr Glu Asn Ser Val Asp Ser Lys Ser Ile Lys Asn Leu
1 5 10 15
Glu Pro Lys Ile Ile His Gly Ser Glu Ser Met Asp Ser Gly Ile Ser
20 25 30
Leu Asp Asn Ser Tyr Lys Met Asp Tyr Pro Glu Met Gly Leu Cys Ile
35 40 45
Ile Ile Asn Asn Lys Asn Phe His Lys Ser Thr Gly Met Thr Ser Arg
50 55 60
Ser Gly Thr Asp Val Asp Ala Ala Asn Leu Arg Glu Thr Phe Arg Asn
65 70 75 80
Leu Lys Tyr Glu Val Arg Asn Lys Asn Asp Leu Thr Arg Glu Glu Ile
85 90 95
Val Glu Leu Met Arg Asp Val Ser Lys Glu Asp His Ser Lys Arg Ser
100 105 110
Ser Phe Val Cys Val Leu Leu Ser His Gly Glu Glu Gly Ile Ile Phe
115 120 125
Gly Thr Asn Gly Pro Val Asp Leu Lys Lys Ile Thr Asn Phe Phe Arg
130 135 140
Gly Asp Arg Cys Arg Ser Leu Thr Gly Lys Pro Lys Leu Phe Ile Ile
145 150 155 160
Gln Ala Cys Arg Gly Thr Glu Leu Asp Cys Gly Ile Glu Thr Asp Ser
165 170 175
Gly Val Asp Asp Asp Met Ala Cys His Lys Ile Pro Val Glu Ala Asp
180 185 190
```

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Phe Leu Tyr Ala Tyr Ser Thr Ala Pro Gly Tyr Tyr Ser Trp Arg Asn
195 200 205
Ser Lys Asp Gly Ser Trp Phe Ile Gln Ser Leu Cys Ala Met Leu Lys
210 215 220
Gln Tyr Ala Asp Lys Leu Glu Phe Met His Ile Leu Thr Arg Val Asn
225 230 235 240
Arg Lys Val Ala Thr Glu Phe Glu Ser Phe Ser Phe Asp Ala Thr Phe
245 250 255
His Ala Lys Lys Gln Ile Pro Cys Ile Val Ser Met Leu Thr Lys Glu
260 265 270
Leu Tyr Phe Tyr His
275

<210> 203
<211> 1906
<212> DNA
<213> Homo sapiens

<400> 203
agaggaaagg gaaggaggag gtcccgaata gcggtcgccg aaatgttccg gtgtggaggc 60
ctggcgccgg gtgctttgaa gcagaagctg gtgcccttgg tgcggaccgt gtgctgccga 120
agcccgaggc agaggaaccg gctcccaggc aacttggtcc agcgaatggc atgttcccta 180
gaactccaga tgacaagaca aatggctagc tctgggtgat cagggggcaa aatcgataat 240
tctgtgttag tccttattgt gggcttatca acagtaggag ctgggtgccta tgcctacaag 300
actatgaaag aggacgaaaa aagatacaat gaaagaattt cagggttagg gctgacacca 360
gaacagaaac agaaaaaggc cgcgttatct gcttcagaag gagaggaggt tcttcaagac 420
aaggcgccaa gtcattgttc tttcctgcta attggtggag gcacagctgc ttttgctgca 480
gccagatcca tccgggctcg ggatcctggg gccagggtac tgattgtatc tgaagatcct 540
gagctgccgt acatgacgac tcctctttca aaagaactgt ggttttcaga tgacccaaat 600
gtcacaaaga cactgagatt caaacagtgg aatggaaaag agagaagcat atatttccag 660
ccaccttctt tctatgtctc tgctcaggac ctgcctcata ttgagaatgg tgggtgtggc 720
gtcctcactg ggaagaaggc agtacagctg gatgtgagag acaacatggg gaaacttaat 780
gatggctctc aaataacctc tgaaaagtgc ttgattgcaa caggaggtag tccaagaagt 840
ctgtctgcca ttgatagggc tggagcagag gtgaagagta gaacaacgct tttcagaaa 900
attggagact ttagaagctt ggagaagatt tcacgggaag tcaaatcaat tacgattatc 960
ggtgggggct tccttggttag cgaactggcc tgtgctcttg gcagaaaggc tgcagccttg 1020
ggcacagaag tgattcaact ctccccgag aaaggaaaata tgggaaagat cctccccgaa 1080
tacctcagca actggaccat ggaaaaagtc agacgagagg ggggttaagg ttatcaagct 1140
gctattgtgc aatccgttgg agtcagcagt ggcaagttac ttatcaagct gaaagacggc 1200
aggaaggtag aaactgacca catagtggca gctgtgggct tggagcccaa tggttgattg 1260
gccaagactg gtggcctgga aatagactca gatattgggt gcttccgggt aaatgcagag 1320
ctacaagcac gctctaactc ctgggtggca ggagatgctg catgcttcta cgaataaag 1380
ttgggaaggc ggcggttaga gcaccatgat cacgctgttg tgagtggaaag attggctgga 1440
gaaaatatga ctggagctgc taagccgtac tggcatcagt caatgttctg gagggtattg 1500
ggccccgatg ttggctatga agctatttgt cttgtggaca gtagtttgcc cacagttggt 1560
gtttttgcaa aagcaactgc acaagacaac cccaaatctg ccacagagca gtcaggaact 1620
ggatccgatg cagagagtgc gacagagtcc gaggcctcag aaattactat tcttccagc 1680
accccgagcag ttccacaggc tcccgtccag ggggaggact acggcaaggg tgtcatcttc 1740
tacctcaggg acaaagtggc cgtggggatt gtgctatgga acatctttaa ccgaatgcca 1800
atagcaaggc agatcattaa ggacggtgag cagcatgaag atctcaatga agtagccaaa 1860
ctattcaaca ttcattgaaga ctgaagcccc acagtggaaat tggcaa 1906

<210> 204
<211> 613
<212> PRT
<213> Homo sapiens

<400> 204
Met Phe Arg Cys Gly Gly Leu Ala Ala Gly Ala Leu Lys Gln Lys Leu
1 5 10 15
Val Pro Leu Val Arg Thr Val Cys Val Arg Ser Pro Arg Gln Arg Asn
20 25 30
Arg Leu Pro Gly Asn Leu Phe Gln Arg Trp His Val Pro Leu Glu Leu
35 40 45
Gln Met Thr Arg Gln Met Ala Ser Ser Gly Ala Ser Gly Gly Lys Ile
50 55 60
Asp Asn Ser Val Leu Val Leu Ile Val Gly Leu Ser Thr Val Gly Ala
65 70 75 80

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Gly Ala Tyr Ala Tyr Lys Thr Met Lys Glu Asp Glu Lys Arg Tyr Asn
85 90 95
Glu Arg Ile Ser Gly Leu Gly Leu Thr Pro Glu Gln Lys Gln Lys Lys
100 105 110
Ala Ala Leu Ser Ala Ser Glu Gly Glu Glu Val Pro Gln Asp Lys Ala
115 120 125
Pro Ser His Val Pro Phe Leu Ile Gly Gly Gly Thr Ala Ala Phe
130 135 140
Ala Ala Ala Arg Ser Ile Arg Ala Arg Asp Pro Gly Ala Arg Val Leu
145 150 155 160
Ile Val Ser Glu Asp Pro Glu Leu Pro Tyr Met Arg Pro Pro Leu Ser
165 170 175
Lys Glu Leu Trp Phe Ser Asp Asp Pro Asn Val Thr Lys Thr Leu Arg
180 185 190
Phe Lys Gln Trp Asn Gly Lys Glu Arg Ser Ile Tyr Phe Gln Pro Pro
195 200 205
Ser Phe Tyr Val Ser Ala Gln Asp Leu Pro His Ile Glu Asn Gly Gly
210 215 220
Val Ala Val Leu Thr Gly Lys Lys Val Val Gln Leu Asp Val Arg Asp
225 230 235 240
Asn Met Val Lys Leu Asn Asp Gly Ser Gln Ile Thr Tyr Glu Lys Cys
245 250 255
Leu Ile Ala Thr Gly Gly Thr Pro Arg Ser Leu Ser Ala Ile Asp Arg
260 265 270
Ala Gly Ala Glu Val Lys Ser Arg Thr Thr Leu Phe Arg Lys Ile Gly
275 280 285
Asp Phe Arg Ser Leu Glu Lys Ile Ser Arg Glu Val Lys Ser Ile Thr
290 295 300
Ile Ile Gly Gly Gly Phe Leu Gly Ser Glu Leu Ala Cys Ala Leu Gly
305 310 315 320
Arg Lys Ala Arg Ala Leu Gly Thr Glu Val Ile Gln Leu Phe Pro Glu
325 330 335
Lys Gly Asn Met Gly Lys Ile Leu Pro Glu Tyr Leu Ser Asn Trp Thr
340 345 350
Met Glu Lys Val Arg Arg Glu Gly Val Lys Val Met Pro Asn Ala Ile
355 360 365
Val Gln Ser Val Gly Val Ser Ser Gly Lys Leu Leu Ile Lys Leu Lys
370 375 380
Asp Gly Arg Lys Val Glu Thr Asp His Ile Val Ala Ala Val Gly Leu
385 390 395 400
Glu Pro Asn Val Glu Leu Ala Lys Thr Gly Gly Leu Glu Ile Asp Ser
405 410 415
Asp Phe Gly Gly Phe Arg Val Asn Ala Glu Leu Gln Ala Arg Ser Asn
420 425 430
Ile Trp Val Ala Gly Asp Ala Ala Cys Phe Tyr Asp Ile Lys Leu Gly
435 440 445
Arg Arg Arg Val Glu His His Asp His Ala Val Val Ser Gly Arg Leu
450 455 460
Ala Gly Glu Asn Met Thr Gly Ala Ala Lys Pro Tyr Trp His Gln Ser
465 470 475 480
Met Phe Trp Ser Asp Leu Gly Pro Asp Val Gly Tyr Glu Ala Ile Gly
485 490 495
Leu Val Asp Ser Ser Leu Pro Thr Val Gly Val Phe Ala Lys Ala Thr
500 505 510
Ala Gln Asp Asn Pro Lys Ser Ala Thr Glu Gln Ser Gly Thr Gly Ile
515 520 525
Arg Ser Glu Ser Glu Thr Glu Ser Glu Ala Ser Glu Ile Thr Ile Pro
530 535 540
Pro Ser Thr Pro Ala Val Pro Gln Ala Pro Val Gln Gly Glu Asp Tyr
545 550 555 560
Gly Lys Gly Val Ile Phe Tyr Leu Arg Asp Lys Val Val Val Gly Ile
565 570 575
Val Leu Trp Asn Ile Phe Asn Arg Met Pro Ile Ala Arg Lys Ile Ile
580 585 590
Lys Asp Gly Glu Gln His Glu Asp Leu Asn Glu Val Ala Lys Leu Phe
595 600 605
Asn Ile His Glu Asp
610

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<210> 205
<211> 1090
<212> DNA
<213> Homo sapiens

```
<400> 205
atggccgctg acaggggacg caggatattg ggagtggtgt gcatgcatcc tcatcatcag 60
gaaactctaa aaaagaaccg agtgggtgcta gccaaacagc tgttggtgag cgaattgtta 120
gaacatcttc tggagaagga catcatcacc ttggaaatga gggagctcat ccaggccaaa 180
gtgggcagtt tcagccagaa tgtggaactc ctcaacttgc tgcctaagag ggggtcccaa 240
gcttttgatg ccttctgtga agccttgac tcctgaattt tatcaaacac acttcagct 300
ggcatatagg ttgcagtctc ggcctcgtgg cctagcactg gtgttgagca atgtgcactt 360
cactggagag aaagaactgg aatttcgctc tggaggggat gtggaccaca gtactctagt 420
caccctcttc aagcttttgg gctatgacgt ccatgttcta tgtgaccaga ctgcacagga 480
aatgcaagag aaactgcaga attttgcaca gttacctgca caccgagtc cggactgctg 540
catcgtggca ctctctcgc atgggtgtgga gggcgccatc tatggtgtgg atgggaaact 600
gctccagctc caagaggttt ttcagctctt tgacaacgcc aaccgcccaa gcctacagaa 660
caaaccacaa atgttcttca tccaggcctg ccgtggagat gagactaatc gtgggggtta 720
ccaacaagat ggaaaagaacc acgcaggatc ccctgggtgc gaggagagtg atgccggtta 780
agaaaagtgt ccgaagatga gactgcccac gcgctcagac atgatatgcg gctatgcctg 840
cctcaaaggg actgccgcca tgcggaacac caaacgaggt tcttggtaca tcgaggctct 900
tgctcaagtg ttttctgagc gggcttgtga tatgcacgtg gccgacatgc tgggttaagg 960
gaacgcactt atcaaggatc gggaaggtaa tgctcctggc acagaattcc accggtgcaa 1020
ggagatgtct gaatactgca gcactctgtg ccgccacctc tacctgttcc caggacacct 1080
tcccacatga                                     1090
```

<210> 206
<211> 91
<212> PRT
<213> Homo sapiens

```
<400> 206
Met Ala Ala Asp Arg Gly Arg Arg Ile Leu Gly Val Cys Gly Met His
 1      5      10      15
Pro His His Gln Glu Thr Leu Lys Lys Asn Arg Val Val Leu Ala Lys
 20      25      30
Gln Leu Leu Leu Ser Glu Leu Leu Glu His Leu Leu Glu Lys Asp Ile
 35      40      45
Ile Thr Leu Glu Met Arg Glu Leu Ile Gln Ala Lys Val Gly Ser Phe
 50      55      60
Ser Gln Asn Val Glu Leu Leu Asn Leu Leu Pro Lys Arg Gly Pro Gln
 65      70      75      80
Ala Phe Asp Ala Phe Cys Glu Ala Leu His Ser
      85      90
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<210> 207
<211> 714
<212> DNA
<213> Artificial Sequence

<220>
<223> Fusion polynucleotide

```
<400> 207
tctgatcagg agcccaaata ttgtgacaaa actcacacat gccaccgtg cccagcacct 60
gaactccttg ggggaccgtc agtcttcttc ttcccccaa aaccacagga caccctcatg 120
atctcccgga ccctgaggtt cacatgcgtg gtggtggacg tgagccacga agaccctgag 180
gtcaagtcca actggtacgt ggacggcgtg gaggtgcata atgccaagac aaagccgagg 240
gaggagcagt acaacagcac gtaccgtgtg gtcagcgtcc tcaccgtcct gcaccaggac 300
tggctgaatg gcaaggagta caagtgcagg gtctccaaca aagccctccc agccccatc 360
gagaaaacaa tctccaaagc caaagggcag ccccgagaac cacagggtga caccctgccc 420
ccatcccggg atgagctgac caagaaccag gtcagcctga cctgcctggt caaaggcttc 480
tatcccagcg acatcgccgt ggagtgggag agcaatgggc agccggagaa caactacaag 540
accacgcctc ccgtgctgga ctccgacggc tccttcttcc tctacagcaa gctcaccgtg 600
gacaagagca ggtggcagca ggggaacgtc ttctcatgct ccgtgatgca tgaggctctg 660
cacaaccact acacgcagaa gagcctctcc ctgtctccgg gtaaatgatc taga 714
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<210> 208
<211> 235
<212> PRT
<213> Artificial Sequence

<220>
<223> Fusion polypeptide

<400> 208
Ser Asp Gln Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro
1 5 10 15
Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro
20 25 30
Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
35 40 45
Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
50 55 60
Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
65 70 75 80
Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
85 90 95
Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
100 105 110
Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
115 120 125
Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
130 135 140
Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
145 150 155 160
Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
165 170 175
Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
180 185 190
Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
195 200 205
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
210 215 220
Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
225 230 235

<210> 209
<211> 718
<212> DNA
<213> Artificial Sequence

<220>
<223> Fusion polynucleotide

<221> misc_feature
<222> 34, 43, 52, 55, 58, 64
<223> n = A,T,C or G

<400> 209
tgatcaagaa ccacatggag gatgcacgtg cccncagtgc ccncaatgcc cngcncnga 60
actnccagga ggcccttctg tctttgtctt ccccccga aa tcctctccat 120
ttttggaggc cgagtcacgt gcgtttagt ggacgtcgga aagaaagacc ccgaggtcaa 180
tttcaactgg tatattgatg gcgttgaggt gcgaacggcc aatacgaagc caaaagagga 240
acagttcaac agcacgtacc gcgtggtcag cgtcctgccc atccagcacc aggactggct 300
gacggggaag gaattcaagt gcaagggtcaa caacaaagct ctcccggccc ccatcgagag 360
gaccatctcc aaggccaaag ggcagaccgc ggagccgcag gtgtacaccc tggccccaca 420
ccgggaagaa ctggccaagg acaccgtgag cgtaacatgc ctgggtcaaag gcttctaccc 480
agctgacatc aacgttgagt ggcagaggaa cggtcagccg gagtcagagg gcacctacgc 540
caacacgccc ccacagctgg acaacgacgg gacctacttc ctctacagca agctctcggg 600
gggaaagaac acgtggcagc ggggagaaac cttaacctgt gtggtgatgc atgaggccct 660
gcacaaccac tacaccaga aatccatcac ccagtcttcg ggtaaatagt aatctaga 718

<210> 210
<211> 757

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<212> DNA

<213> Artificial Sequence

<220>

<223> Fusion polynucleotide

<400> 210

tgatcaagaa	cccaagacac	caaaaccaca	accacaa cca	caaccacaac	ccaatcctac	60
aacagaatcc	aagtgtccca	aatgtccagc	ccctgagctc	ctgggagggc	cctcagtctt	120
catcttcccc	ccgaaaccca	aggacgtcct	ctccatttct	gggaggcccg	aggtcacgtg	180
cggtgtggtg	gacgtgggcc	aggaagaccc	cgaggtcagt	ttcaactggg	acattgatgg	240
cgctgaggtg	cgaacggcca	acacgaggcc	aaaagaggaa	cagttcaaca	gcacgtaccg	300
cggtgtcagc	gtcctgcccc	tccagcacca	ggactggctg	acggggaagg	aattcaagtg	360
caaggtcaac	aacaaagctc	tcccggcccc	catcgagaag	accatctcca	aggccaaagg	420
gcagaccggg	gagccgcagg	tgtacaccct	ggcccca cac	cggaagagc	tggccaagga	480
caccgtgagc	gtaacatgcc	tggtcaaagg	cttctaccca	cctgatatca	acgttgagtg	540
gcagaggaat	gggcagccgg	agtcagaggg	cacytacgcc	accacgccac	cccagctgga	600
caacgacggg	acctacttcc	tctacagcaa	gctctcggtg	ggaaagaaca	cgtggcagca	660
gggagaaacc	ttcacctgtg	tggtgatgca	cgaggccctg	cacaaccact	acaccagaa	720
atccatcacc	cagtcttcgg	gtaaatagta	atctaga			757

<210> 211

<211> 727

<212> DNA

<213> Artificial Sequence

<220>

<223> Fusion polynucleotide

<400> 211

tgatcaagcg	caccacagcg	aagaccccg	ctccaagtgt	cccaaatgcc	caggccctga	60
actccttggg	gggcccacgg	tcttcatctt	ccccccgaaa	gccaaaggacg	tcctctccat	120
cacccgaaaa	cctgaggtca	cggtgttggt	gtggacgtgg	gtaaagaaga	ccctgagatc	180
gagttcaagc	tggtccgtgg	atgacacaga	ggtacacacg	gctgagacaa	agccaaagga	240
ggaacagttc	aacagcacgt	accgcgtggt	cagcgtcctg	cccattccagc	accaggactg	300
gctgacgggg	aaggaattca	agtgcagggt	caacaacaaa	gctctcccag	cccccatcga	360
gaggaccatc	tccaaggcca	aagggcagac	ccgggagccg	caggtgtaca	ccctggcccc	420
acaccgggaa	gagctggcca	aggacaccgt	gagcgttaac	tgcctggtca	aaggcttctt	480
cccagctgac	atcaacgttg	agtggcagag	gaatgggcag	ccggagtcag	agggcaccta	540
cgccaacacg	ccgccacagc	tggaacaacga	cgggacctac	ttcctctaca	gcaaactctc	600
cggtgggaaag	aacacgtggc	agcagggaga	agtcttcacc	tgtgtggtga	tgacagaggc	660
tctacacaat	cactccaccc	agaaatccat	caccagctct	tcgggtaaat	agtaatctag	720
agggcc						727

<210> 212

<211> 231

<212> PRT

<213> Artificial Sequence

<220>

<223> Fusion polypeptide

<400> 212

Glu	Pro	His	Gly	Gly	Cys	Thr	Cys	Pro	Gln	Cys	Pro	Ala	Pro	Glu	Leu
1				5					10					15	
Pro	Gly	Gly	Pro	Ser	Val	Phe	Val	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Val
			20					25					30		
Leu	Ser	Ile	Ser	Gly	Arg	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val
		35					40					45			
Gly	Lys	Glu	Asp	Pro	Glu	Val	Asn	Phe	Asn	Trp	Tyr	Ile	Asp	Gly	Val
	50				55					60					
Glu	Val	Arg	Thr	Ala	Asn	Thr	Lys	Pro	Lys	Glu	Glu	Gln	Phe	Asn	Ser
	65				70					75				80	
Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Pro	Ile	Gln	His	Gln	Asp	Trp	Leu
			85					90					95		
Thr	Gly	Lys	Glu	Phe	Lys	Cys	Lys	Val	Asn	Asn	Lys	Ala	Leu	Pro	Ala
			100					105					110		
Pro	Ile	Glu	Arg	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Thr	Arg	Glu	Pro
	115						120					125			

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
 Gln Val Tyr Thr Leu Ala Pro His Arg Glu Glu Leu Ala Lys Asp Thr
 130 135 140
 Val Ser Val Thr Cys Leu Val Lys Gly Phe Tyr Pro Ala Asp Ile Asn
 145 150 155 160
 Val Glu Trp Gln Arg Asn Gly Gln Pro Glu Ser Glu Gly Thr Tyr Ala
 165 170 175
 Asn Thr Pro Pro Gln Leu Asp Asn Asp Gly Thr Tyr Phe Leu Tyr Ser
 180 185 190
 Arg Leu Ser Val Gly Lys Asn Thr Trp Gln Arg Gly Glu Thr Leu Thr
 195 200 205
 Gly Val Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
 210 215 220
 Ile Thr Gln Ser Ser Gly Lys
 225 230

<210> 213
 <211> 248
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Fusion polypeptide

<400> 213
 Asp Gln Glu Pro Lys Thr Pro Lys Pro Gln Pro Gln Pro Gln Pro Gln
 1 5 10 15
 Pro Asn Pro Thr Thr Glu Ser Lys Cys Pro Lys Cys Pro Ala Pro Glu
 20 25 30
 Leu Leu Gly Gly Pro Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp
 35 40 45
 Val Leu Ser Ile Ser Gly Arg Pro Glu Val Thr Cys Val Val Asp
 50 55 60
 Val Gly Gln Glu Asp Pro Glu Val Ser Phe Asn Trp Tyr Ile Asp Gly
 65 70 75 80
 Ala Glu Val Arg Thr Ala Asn Thr Arg Pro Lys Glu Glu Gln Phe Asn
 85 90 95
 Ser Thr Tyr Arg Val Val Ser Val Leu Pro Ile Gln His Gln Asp Trp
 100 105 110
 Leu Thr Gly Lys Glu Phe Lys Cys Lys Val Asn Asn Lys Ala Leu Pro
 115 120 125
 Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Thr Arg Glu
 130 135 140
 Pro Gln Val Tyr Thr Leu Ala Pro His Arg Glu Glu Leu Ala Lys Asp
 145 150 155 160
 Thr Val Ser Val Thr Cys Leu Val Lys Gly Phe Tyr Pro Pro Asp Ile
 165 170 175
 Asn Val Glu Trp Gln Arg Asn Gly Gln Pro Glu Ser Glu Gly Thr Tyr
 180 185 190
 Ala Thr Thr Pro Pro Gln Leu Asp Asn Asp Gly Thr Tyr Phe Leu Tyr
 195 200 205
 Ser Lys Leu Ser Val Gly Lys Asn Thr Trp Gln Gln Gly Glu Thr Phe
 210 215 220
 Thr Cys Val Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
 225 230 235 240
 Ser Ile Thr Gln Ser Ser Gly Lys
 245

<210> 214
 <211> 236
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Fusion polypeptide

<400> 214
 Asp Gln Ala His His Ser Glu Asp Pro Ser Ser Lys Cys Pro Lys Cys

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
 1 5 10 15
 Pro Gly Pro Glu Leu Leu Gly Gly Pro Thr Val Phe Ile Phe Pro Pro
 20 25 30
 Lys Ala Lys Asp Val Leu Ser Ile Thr Arg Lys Pro Glu Val Thr Cys
 35 40 45
 Leu Trp Trp Thr Trp Val Lys Thr Leu Arg Ser Ser Ser Ser Trp
 50 55 60
 Ser Val Asp Asp Thr Glu Val His Thr Ala Glu Thr Lys Pro Lys Glu
 65 70 75 80
 Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Pro Ile Gln
 85 90 95
 His Gln Asp Trp Leu Thr Gly Lys Glu Phe Lys Cys Lys Val Asn Asn
 100 105 110
 Lys Ala Leu Pro Ala Pro Ile Glu Arg Thr Ile Ser Lys Ala Lys Gly
 115 120 125
 Gln Thr Arg Glu Pro Gln Val Tyr Thr Leu Ala Pro His Arg Glu Glu
 130 135 140
 Leu Ala Lys Asp Thr Val Ser Val Thr Cys Leu Val Lys Gly Phe Phe
 145 150 155 160
 Pro Ala Asp Ile Asn Val Glu Trp Gln Arg Asn Gly Gln Pro Glu Ser
 165 170 175
 Glu Gly Thr Tyr Ala Asn Thr Pro Pro Gln Leu Asp Asn Asp Gly Thr
 180 185 190
 Tyr Phe Leu Tyr Ser Lys Leu Ser Val Gly Lys Asn Thr Trp Gln Gln
 195 200 205
 Gly Glu Val Phe Thr Cys Val Val Met His Glu Ala Leu His Asn His
 210 215 220
 Ser Thr Gln Lys Ser Ile Thr Gln Ser Ser Gly Lys
 225 230 235

<210> 215
 <211> 54
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Fusion polynucleotide

<400> 215
 gatcaggagc ccaaattcttg tgacaaaact cacacatgcc caCcggtgccc agca 54

<210> 216
 <211> 18
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Fusion polypeptide

<400> 216
 Asp Gln Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
 1 5 10 15
 Pro Ala

<210> 217
 <211> 54
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Fusion polynucleotide

<400> 217
 gatctggagc ccaaattcttg tgacaaaact cacacatgcc cacCgtgccc agca 54

<210> 218

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<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Fusion polypeptide

<400> 218
Asp Leu Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
1 5 10 15
Pro Ala

<210> 219
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Fusion polynucleotide

<400> 219
cctgaactcc tgggggggacc gtcagtcttc ctcttcccc caaaacccaa ggacaccctc 60
atgatctccc ggaccctga ggtcacatgc gtggtggtgg acgtgagcca cgaagaccct 120
gaggtcaagt tcaactggt cgtggacggc gtggaggtgc ataatgcca gacaaagccg 180
cgggaggagc agtacaacag cacgtaccgt gtggtcagcg tcctcaccgt cctgcaccag 240
gactggctga atggcaagga gtacaagtgc aaggctctca acaaagccct cccagccccc 300
atcgagaaaa ccattctcaa agccaaa 327

<210> 220
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Fusion polypeptide

<400> 220
Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
1 5 10 15
Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
20 25 30
Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
35 40 45
Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
50 55 60
Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
65 70 75 80
Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
85 90 95
Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
100 105

<210> 221
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> Fusion polynucleotide

<400> 221
gggcagcccc gagaaccaca ggtgtacacc ctgcccccat cccgggagga gatgaccaag 60
aaccaggtca gcctgacctg cctggtcaaa ggcttctatc ccagcgacat cgccgtggag 120
tgggagagca atgggcagcc ggagaacaac tacaagacca cgcctcccgt gctggactcc 180
gacggctcct tcttctctta tagcaagctc accgtggaca agagcaggtg gcagcagggg 240
aacgtcttct catgctccgt gatgcatgag gctctgcaca accactacac gcagaagagc 300

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt 324
ctctccctgt ccccggttaa atga

<210> 222
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Fusion polypeptide

<400> 222
Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu
1 5 10 15
Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
20 25 30
Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
35 40 45
Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
50 55 60
Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
65 70 75 80
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
85 90 95
Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
100 105

<210> 223
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Fusion polynucleotide

<400> 223
gatcaggagc ccaaattcttc tgacaaaact cacacatccc caccgtcccc agca 54

<210> 224
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Fusion polypeptide

<400> 224
Asp Gln Glu Pro Lys Ser Ser Asp Lys Thr His Thr Ser Pro Pro Ser
1 5 10 15
Pro Ala

<210> 225
<211> 712
<212> DNA
<213> Artificial Sequence

<220>
<223> Fusion polynucleotide

<400> 225
tgatcacccc aaattcttctg acaaaactca cacatctcca ccgtcctcag cacctgaact 60
cctgggtgga ccgtcagtct tcctcttccc cccaaaaccc aaggacacc tcatgatctc 120
ccggaccctt gaggtcacat gcgtgggtgg ggacgtgagc cacgaagacc ctgaggtcaa 180
gttcaactgg tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgcgggagga 240

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gcagtacaac agcacgtacc gtgtggtcag cgtcctcacc gtcctgcacc aggactggct 300
gaatggcaag gagtacaagt gcaaggtctc caacaaagcc ctcccagccc ccatcgagaa 360
aacaatctcc aaagccaaag ggcagcccg agaaccacag gtgtacaccc tgcccccatc 420
ccgggatgag ctgaccaaga accaggtcag cctgacctgc ctgggtcaaag gcttctatcc 480
cagcgacatc gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac 540
gcctcccgtg ctggactccg acggctcctt cttcctctac agcaagctca ccgtggacaa 600
gagcaggtgg cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa 660
ccactacacg cagaagagcc tctccctgtc tccgggtaaa tgataatcta ga 712

<210> 226
<211> 233
<212> PRT
<213> Artificial Sequence

<220>
<223> Fusion polypeptide

<400> 226
Asp His Pro Lys Ser Ser Asp Lys Thr His Thr Ser Pro Pro Ser Ser
1 5 10 15
Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
20 25 30
Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
35 40 45
Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
50 55 60
Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
65 70 75 80
Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
85 90 95
Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
100 105 110
Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
115 120 125
Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
130 135 140
Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
145 150 155 160
Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
165 170 175
Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
180 185 190
Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
195 200 205
Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
210 215 220
Lys Ser Leu Ser Leu Ser Pro Gly Lys
225 230

<210> 227
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> 5' primer for llama IgG1 constant region

<400> 227
gtgttgatc aagaaccaca tggaggatgc acgtg

35

<210> 228
<211> 32
<212> DNA
<213> Artificial Sequence

<220>

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<223> 5' primer for llama IgG2 constant region

<400> 228
gttggtgatc aagaacccaa gacacaaaa cc 32

<210> 229
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> 5' primer for llama IgG3 constant region

<400> 229
gttggtgatc aagcgcacca cagcgaagac ccc 33

<210> 230
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Llama Fc sense sequencing primer

<400> 230
ctgagatcga gtccagctg 19

<210> 231
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Llama Fc antisense sequencing primer

<400> 231
cctcctttgg ctttgtctc 19

<210> 232
<211> 1527
<212> DNA
<213> Artificial Sequence

<220>
<223> fusion polynucleotide

<221> misc_feature
<222> 843, 852, 861, 864, 867, 873
<223> n = A,T,C or G

<400> 232
aagcttgccg ccatggattt tcaagtgcag attttcagct tcctgctaata cagtgccttca 60
gtcataattg ccagaggaca aattgtcttc tcccagcttc cagcaatcct gtctgcatct 120
ccaggggaga aggtcaccaat gacttgcagg gccagctcaa gtgtaagtta catgcactgg 180
taccagcaga agccaggatc ctccccaaa ccctggattt atgccccatc caacctggct 240
tctggagtcc ctgctcgctt cagtggcagt gggtctggga cctcttactc tctcacaatc 300
agcagagtgg aggtgaaga tgctgccact tattactgcc agcagtggag ttttaaccca 360
cccacgttcg gtgctgggac caagctggag ctgaaagatg gcggtgggctc gggcggtggg 420
ggatctggag gaggtgggag ctctcaggct tatctacagc agtctggggc tgagctgggtg 480
aggcctgggg cctcagtgaa gatgtcctgc aaggcttctg gctacacatt taccagttac 540
aatatgcact gggtaaagca gacacctaga cagggcctgg aatggattgg agctatttat 600
ccaggaaatg gtgatacttc ctacaatcag aagttcaagg gcaaggccac actgactgta 660
gacaaatcct ccagcacagc ctacatgcag ctacagagcc tgacatctga agactctgctg 720
gtctatttct gtgcaagagt ggtgtactat agtaactctt actgggtactt cgatgtctgg 780
ggcacaggga ccacgggtcac cgtctcttct gatcaagaac cacatggagg atgcacgtgc 840

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
 ccncagtgcc cncaatgccc ngcncengaa ctncaggag gcccttctgt ctttgtcttc 900
 cccccgaaac ccaaggacgt cctctccatt tttggaggcc gagtcacgtg cgttgtagtg 960
 gacgtcggaa agaaagacc cgaggtcaat ttcaactggt atattgatgg cgttgaagg 1020
 cgaacggcca atacgaagcc aaaagaggaa cagttcaaca gcacgtaccg cgttgtcagc 1080
 gtctgcccc tccagcacca ggactggctg acggggaagg aattcaagtg caaggtcaac 1140
 aacaaagctc tcccggcccc catcgagagg accatctcca aggccaaagg gcagacccgg 1200
 gagccgcagg tgtacaccct ggccccacac cgggaagaac tggccaagga caccgtgagc 1260
 gtaacatgcc tgggtcaaagg cttctaccca gctgacatca acgttgagtg gcagaggaac 1320
 ggtagccgg agtcagaggg cacctacgcc aacacgccgc cacagctgga caacgaagg 1380
 acctacttcc tctacagcaa gctctcggtg ggaaagaaca cgtggcagcg gggagaacc 1440
 ttaacctgtg tgggtgatga tgaggccctg cacaaccact acaccagaa atccatcacc 1500
 cagtcttcgg gtaaatagta atctaga 1527

<210> 233
 <211> 1566
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> fusion polynucleotide

<400> 233
 aagcttgccg ccatggattt tcaagtgcag attttcagct tcctgctaata cagtgccttca 60
 gtcataattg ccagaggaca aattgttctc tcccagctctc cagcaatcct gtctgcatct 120
 ccaggggaga aggtcacaaat gacttgcagg gccagctcaa gtgtaagtta catgcactgg 180
 taccagcaga agccaggatc ctccccaaa ccctggattt atgccccatc caacctggct 240
 tctggagtcct ctgctcgctt cagtggcagt gggctctggga cctcttactc tctcacaatc 300
 agcagagtgg aggtgaaga tgctgccact tattactgcc agcagtggag ttttaacca 360
 cccacgttcg gtgctgggac caagctggag ctgaaagatg gcggtggctc gggcggtggt 420
 ggatctggag gaggtgggag ctctcaggct tatctacagc agtctggggc tgagctggg 480
 aggcctgggg cctcagtga gatgtcctgc aaggcttctg gctacacatt taccagttac 540
 aatatgcact gggtaaagca gacacctaga cagggcctgg aatggattgg agctatttat 600
 ccaggaatag gtgatacttc ctacaatcag aagttaagg gcaaggccac actgactgta 660
 gacaaatcct ccagcacagc ctacatgcag ctacagagcc tgacatctga agactctgcg 720
 gtctatttct gtgcaagagt ggtgtactat agtaactctt actggctact cgatgtctgg 780
 ggcacaggga ccacggtcac cgtctcttct gatcaagaac ccaagacacc aaaacca 840
 ccacaaccac aaccacaacc caatctaca acagaatcca agtgtcccaa atgtccagcc 900
 cctgagctcc tgggagggcc ctcagctctc atcttcccc cgaaccccaa ggacgtctc 960
 tccatttctg ggaggccga ggtcacgtgc gctgggctgg aatggattgg ggaagacccc 1020
 gaggtcagtt tcaactggta cattgatggc cctgaggtgc gaacggccaa cagcaggcca 1080
 aaagaggaac agttcaacag caggtaccgc gtggtcagcg tcctgcccac ccagcacca 1140
 gactggctga cggggaagga attcaagtgc aagggtcaaca acaagctct cccggccc 1200
 atcgagaaga ccatctccaa ggccaaaggg cagacccggg agccgcaggt gtacaccctg 1260
 gccccacacc ggaagagct ggccaaaggc accgtgagcg taacatgcct ggtcaaaagg 1320
 ttctacccac ctgatataca cgttgagtgg cagaggaatg ggcagccgga gtcagaggc 1380
 acytacgcca ccacgccacc ccagctggag aacgacggga cctacttcct ctacagcaag 1440
 ctctcggtgg gaaagaacac gtggcagcag ggagaaacct tcacctgtgt ggtgatgac 1500
 gaggccctgc acaaccacta caccagaaa tccatcacc agtcttcggg taaatagtaa 1566
 tctaga 1566

<210> 234
 <211> 1536
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> fusion polynucleotide

<400> 234
 aagcttgccg ccatggattt tcaagtgcag attttcagct tcctgctaata cagtgccttca 60
 gtcataattg ccagaggaca aattgttctc tcccagctctc cagcaatcct gtctgcatct 120
 ccaggggaga aggtcacaaat gacttgcagg gccagctcaa gtgtaagtta catgcactgg 180
 taccagcaga agccaggatc ctccccaaa ccctggattt atgccccatc caacctggct 240
 tctggagtcct ctgctcgctt cagtggcagt gggctctggga cctcttactc tctcacaatc 300
 agcagagtgg aggtgaaga tgctgccact tattactgcc agcagtggag ttttaacca 360
 cccacgttcg gtgctgggac caagctggag ctgaaagatg gcggtggctc gggcggtggt 420
 ggatctggag gaggtgggag ctctcaggct tatctacagc agtctggggc tgagctggg 480
 aggcctgggg cctcagtga gatgtcctgc aaggcttctg gctacacatt taccagttac 540
 aatatgcact gggtaaagca gacacctaga cagggcctgg aatggattgg agctatttat 600

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 ccaggaaatg gtgatacttc ctacaatcag aagttcaagg gcaaggccac actgactgta 660
 gacaaatcct ccagcacagc ctacatgcag ctcagcagcc tgacatctga agactctgcg 720
 gtctatttct gtgcaagagt ggtgtactat agtaactctt actggtactt cgatgtctgg 780
 ggcacagggg ccacgggtcac cgtctcttct gatcaagcga accacagcga agaccccagc 840
 tccaagtgtc ccaaagtcgc agggccctgaa ctctctggag ggcccacggt cttcatcttc 900
 cccccgaaag ccaaggacgt cctctccatc acccgaaaac ctgaggtcac gtgcttgtgg 960
 tggacgtggg taaagaagac cctgagatcg agttcaagct ggtccgtgga tgacacagag 1020
 gtacacacgg ctgagacaaa gccaaaggag gaacagtcca acagcacgta ccgcgtgggtc 1080
 agcgtcctgc ccatccagca ccaggactgg ctgacgggga aggaattcaa gtgcaaggctc 1140
 aacaacaaag ctctcccagc ccccatcgag aggaccatct ccaaggccaa agggcagacc 1200
 cgggagccgc aggtgtacac cctggcccca caccgggaag agctggccaa ggacaccgtg 1260
 agcgtaacct gcctgggtcaa aggcctcttc ccagctgaca tcaacgttga gtggcagagg 1320
 aatgggcagc cggagtcaga gggcacctac gccaacacgc cgccacagct ggacaacgac 1380
 gggacctact tcctctacag caaactctcc gtgggaaaga acacgtggca gcaggggagaa 1440
 gtcttcacct gtgtggtgat gcacgaggct ctacacatc actccacca gaaatccatc 1500
 acccagtctt cgggtaaata gtaatctaga gggccc 1536

<210> 235
 <211> 498
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> fusion polypeptide

<400> 235
 Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1 5 10 15
 Val Ile Ile Ala Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile
 20 25 30
 Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser
 35 40 45
 Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser
 50 55 60
 Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro
 65 70 75 80
 Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
 85 90 95
 Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
 100 105 110
 Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
 115 120 125
 Asp Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Ser
 130 135 140
 Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala
 145 150 155 160
 Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
 165 170 175
 Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile
 180 185 190
 Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
 195 200 205
 Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
 210 215 220
 Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
 225 230 235 240
 Ala Arg Val Val Tyr Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp
 245 250 255
 Gly Thr Gly Thr Thr Val Thr Val Ser Ser Asp Gln Glu Pro His Gly
 260 265 270
 Gly Cys Thr Cys Pro Gln Cys Pro Ala Pro Glu Leu Pro Gly Gly Pro
 275 280 285
 Ser Val Phe Val Phe Pro Pro Lys Pro Lys Asp Val Leu Ser Ile Phe
 290 295 300
 Gly Gly Arg Val Thr Cys Val Val Val Asp Val Gly Lys Lys Asp Pro
 305 310 315 320
 Glu Val Asn Phe Asn Trp Tyr Ile Asp Gly Val Glu Val Arg Thr Ala
 325 330 335
 Asn Thr Lys Pro Lys Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
 340 345 350
 Ser Val Leu Pro Ile Gln His Gln Asp Trp Leu Thr Gly Lys Glu Phe
 355 360 365
 Lys Cys Lys Val Asn Asn Lys Ala Leu Pro Ala Pro Ile Glu Arg Thr
 370 375 380
 Ile Ser Lys Ala Lys Gly Gln Thr Arg Glu Pro Gln Val Tyr Thr Leu
 385 390 395 400
 Ala Pro His Arg Glu Glu Leu Ala Lys Asp Thr Val Ser Val Thr Cys
 405 410 415
 Leu Val Lys Gly Phe Tyr Pro Ala Asp Ile Asn Val Glu Trp Gln Arg
 420 425 430
 Asn Gly Gln Pro Glu Ser Glu Gly Thr Tyr Ala Asn Thr Pro Gln
 435 440 445
 Leu Asp Asn Asp Gly Thr Tyr Phe Leu Tyr Ser Lys Leu Ser Val Gly
 450 455 460
 Lys Asn Thr Trp Gln Arg Gly Glu Thr Leu Thr Cys Val Val Met His
 465 470 475 480
 Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Ile Thr Gln Ser Ser
 485 490 495
 Gly Lys

<210> 236
 <211> 514
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> fusion polypeptide

<400> 236
 Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1 5 10 15
 Val Ile Ile Ala Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile
 20 25 30
 Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser
 35 40 45
 Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser
 50 55 60
 Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro
 65 70 75 80
 Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
 85 90 95
 Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
 100 105 110
 Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
 115 120 125
 Asp Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser
 130 135 140
 Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala
 145 150 155 160
 Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
 165 170 175
 Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile
 180 185 190
 Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
 195 200 205
 Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Thr Ala Tyr
 210 215 220
 Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
 225 230 235 240
 Ala Arg Val Val Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp
 245 250 255
 Gly Thr Gly Thr Thr Val Thr Val Ser Ser Asp Gln Glu Pro Lys Thr
 260 265 270
 Pro Lys Pro Gln Pro Gln Pro Gln Pro Gln Pro Asn Pro Thr Thr Glu
 275 280 285
 Ser Lys Cys Pro Lys Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser

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290	Val	Phe	Ile	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Val	Leu	Ser	Ile	Ser	Gly
305	Arg	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Gly	Gln	Glu	Asp	Pro
	Glu	Val	Ser	Phe	Asn	Trp	Tyr	Ile	Asp	Gly	Ala	Glu	Val	Arg	Thr	Ala
	Asn	Thr	Arg	Pro	Lys	Glu	Glu	Gln	Phe	Asn	Ser	Thr	Tyr	Arg	Val	Val
	Ser	Val	Leu	Pro	Ile	Gln	His	Gln	Asp	Trp	Leu	Thr	Gly	Lys	Glu	Phe
	Lys	Cys	Lys	Val	Asn	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr
385	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Thr	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu
	Ala	Pro	His	Arg	Glu	Glu	Leu	Ala	Lys	Asp	Thr	Val	Ser	Val	Thr	Cys
	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Pro	Asp	Ile	Asn	Val	Glu	Trp	Gln	Arg
	Asn	Gly	Gln	Pro	Glu	Ser	Glu	Gly	Thr	Tyr	Ala	Thr	Thr	Pro	Pro	Gln
	Leu	Asp	Asn	Asp	Gly	Thr	Tyr	Phe	Leu	Tyr	Ser	Lys	Leu	Ser	Val	Gly
465	Lys	Asn	Thr	Trp	Gln	Gln	Gly	Glu	Thr	Phe	Thr	Cys	Val	Val	Met	His
	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Ile	Thr	Gln	Ser	Ser
	Gly	Lys														

<210> 237
<211> 503
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion polypeptide

<400> 237

Met	Asp	Phe	Gln	Val	Gln	Ile	Phe	Ser	Phe	Leu	Leu	Ile	Ser	Ala	Ser
1				5					10					15	
Val	Ile	Ile	Ala	Arg	Gly	Gln	Ile	Val	Leu	Ser	Gln	Ser	Pro	Ala	Ile
			20					25					30		
Leu	Ser	Ala	Ser	Pro	Gly	Glu	Lys	Val	Thr	Met	Thr	Cys	Arg	Ala	Ser
		35					40					45			
Ser	Ser	Val	Ser	Tyr	Met	His	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Ser	Ser
	50					55					60				
Pro	Lys	Pro	Trp	Ile	Tyr	Ala	Pro	Ser	Asn	Leu	Ala	Ser	Gly	Val	Pro
65				70					75					80	
Ala	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Ser	Tyr	Ser	Leu	Thr	Ile
			85						90					95	
Ser	Arg	Val	Glu	Ala	Glu	Asp	Ala	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Trp
			100					105					110		
Ser	Phe	Asn	Pro	Pro	Thr	Phe	Gly	Ala	Gly	Thr	Lys	Leu	Glu	Leu	Lys
		115					120					125			
Asp	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Ser
	130					135						140			
Gln	Ala	Tyr	Leu	Gln	Gln	Ser	Gly	Ala	Glu	Leu	Val	Arg	Pro	Gly	Ala
145				150					155					160	
Ser	Val	Lys	Met	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Thr	Ser	Tyr
			165						170					175	
Asn	Met	His	Trp	Val	Lys	Gln	Thr	Pro	Arg	Gln	Gly	Leu	Glu	Trp	Ile
		180						185					190		
Gly	Ala	Ile	Tyr	Pro	Gly	Asn	Gly	Asp	Thr	Ser	Tyr	Asn	Gln	Lys	Phe
		195					200					205			
Lys	Gly	Lys	Ala	Thr	Leu	Thr	Val	Asp	Lys	Ser	Ser	Ser	Thr	Ala	Tyr
	210					215					220				
Met	Gln	Leu	Ser	Ser	Leu	Thr	Ser	Glu	Asp	Ser	Ala	Val	Tyr	Phe	Cys

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
225      230      235      240
Ala Arg Val Val Tyr Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp
      245
Gly Thr Gly Thr Val Thr Val Ser Ser Asp Gln Ala His Ser His
      250
Ser Glu Asp Pro Ser Ser Lys Cys Pro Lys Cys Pro Gly Pro Glu Leu
      255
Leu Gly Gly Pro Thr Val Phe Ile Phe Pro Pro Lys Ala Lys Asp Val
      260
Leu Ser Ile Thr Arg Lys Pro Glu Val Thr Cys Leu Trp Trp Thr Trp
      265
Val Lys Lys Thr Leu Arg Ser Ser Ser Ser Trp Ser Val Asp Asp Thr
      270
Glu Val His Thr Ala Glu Thr Lys Pro Lys Glu Glu Gln Phe Asn Ser
      275
Thr Tyr Arg Val Val Ser Val Leu Pro Ile Gln His Gln Asp Trp Leu
      280
Thr Gly Lys Glu Phe Lys Cys Lys Val Asn Asn Lys Ala Leu Pro Ala
      285
Pro Ile Glu Arg Thr Ile Ser Lys Ala Lys Gly Gln Thr Arg Glu Pro
      290
Gln Val Tyr Thr Leu Ala Pro His Arg Glu Glu Leu Ala Lys Asp Thr
      295
Val Ser Val Thr Cys Leu Val Lys Gly Phe Phe Pro Ala Asp Ile Asn
      300
Val Glu Trp Gln Arg Asn Gly Gln Pro Glu Ser Glu Gly Thr Tyr Ala
      305
Asn Thr Pro Pro Gln Leu Asp Asn Asp Gly Thr Tyr Phe Leu Tyr Ser
      310
Lys Leu Ser Val Gly Lys Asn Thr Trp Gln Gln Gly Glu Val Phe Thr
      315
Cys Val Val Met His Glu Ala Leu His Asn His Ser Thr Gln Lys Ser
      320
Ile Thr Gln Ser Ser Gly Lys
      325
      330
      335
      340
      345
      350
      355
      360
      365
      370
      375
      380
      385
      390
      395
      400
      405
      410
      415
      420
      425
      430
      435
      440
      445
      450
      455
      460
      465
      470
      475
      480
      485
      490
      495
      500

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<210> 238
<211> 42
<212> DNA
<213> Artificial Sequence

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<220>
<223> 3'-primer for llama IgG1, IgG2, IgG3 constant
      region

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<400> 238
gtgttttcta gattactatt tacccgaaga ctgggtgatg ga

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42

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<210> 239
<211> 1521
<212> DNA
<213> Artificial Sequence

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<220>
<223> fusion polynucleotide

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<400> 239
aagcttgccg ccatggattt tcaagtgcag attttcagct tcctgctaatt cagtgtttca 60
gtcataattg ccagaggaca aattgttctc tcccagtcct cagcaatcct gtctgcatct 120
ccaggggaga aggtcacaat gacttgcagg gccagctcaa gtgtaagtta catgcactgg 180
taccagcaga agccaggatc ctccccaaa ccctggattt atgccccatc caacctgggt 240
tctggagtcc ctgtcgcgtt cagtggcagt gggctctggga cctcttactc tctcacaatc 300
agcagagtgg aggtgaaga tgctgccact tattactgcc agcagtggag ttttaaccac 360
ccacagttcg gtgctgggac caagctggag ctgaaagatg gcggtggctc gggcggtggg 420
ggatctggag gagtgaggag ctctcaggct tatctacagc agtctggggc tgagctgggt 480
aggcctgggg cctcagtgaat gatgtcctgc aaggcttctg gctacacatt taccagttac 540
aatatgcact ggttaaagca gacacctaga cagggcctgg aatggattgg agctatttat 600
ccaggaaatg gtgatacttc ctacaatcag aagtccaagg gcaaggccac actgactgta 660

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
gacaaatcct ccagcacagc ctacatgcag ctcagcagcc tgacatctga agactctgcg 720
gtctatttct gtgcaagagt ggtgtactat agtaactctt actggtactt cgatgtctgg 780
ggcacaggga ccacggtcac cgtctcttct gatcaggagc ccaaactcttg tgacaaaact 840
cacacatgcc caccgtgccc agcacctgaa ctctctgggg gaccgtcagt cttcctcttc 900
ccccaaaaac ccaaggacac cctcatgata tcccggaccc ctgaggtcac atgcgtgggtg 960
gtggacgtga gccacgaaga ccctgagggtc aagtccaact ggtacgtgga cggcgtggag 1020
gtgcataatg ccaagacaaa gccgcgggag gaggcagtag acagcacgta ccgtgtgggtc 1080
agcgtcctca ccgtcctgca ccaggactgg ctgaatggca aggagtacaa gtgcaagggtc 1140
tccaacaaag cctcccagc ccccatcgag aaaacaatct ccaaagccaa agggcagccc 1200
cgagaaccac aggtgtacac cctgccccca tcccgggatg agctgaccaa gaaccagggtc 1260
agcgtgacct gcctgggtcaa aggccttctat cccagcgaca tcgcccgtgga gtggggagagc 1320
aatgggcagc cggagaacaa ctacaagacc agcgtctccg tgctggactc cgacgggtcc 1380
ttcttcctct acagcaagct caccgtggac aagagcaggt ggcagcaggg gaacgtcttc 1440
tcatgctccg tgatgcatga ggctctgcac aaccactaca cgcagaagag cctctccctg 1500
tctccgggta aatgatctag a 1521

<210> 240

<211> 500

<212> PRT

<213> Artificial Sequence

<220>

<223> fusion polypeptide

<400> 240

Met	Asp	Phe	Gln	Val	Gln	Ile	Phe	Ser	Phe	Leu	Leu	Ile	Ser	Ala	Ser
1				5					10					15	
Val	Ile	Ile	Ala	Arg	Gly	Gln	Ile	Val	Leu	Ser	Gln	Ser	Pro	Ala	Ile
			20					25					30		
Leu	Ser	Ala	Ser	Pro	Gly	Glu	Lys	Val	Thr	Met	Thr	Cys	Arg	Ala	Ser
		35					40					45			
Ser	Ser	Val	Ser	Tyr	Met	His	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Ser	Ser
	50					55					60				
Pro	Lys	Pro	Trp	Ile	Tyr	Ala	Pro	Ser	Asn	Leu	Ala	Ser	Gly	Val	Pro
65				70					75					80	
Ala	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Ser	Tyr	Ser	Leu	Thr	Ile
			85						90					95	
Ser	Arg	Val	Glu	Ala	Glu	Asp	Ala	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Trp
			100				105						110		
Ser	Phe	Asn	Pro	Pro	Thr	Phe	Gly	Ala	Gly	Thr	Lys	Leu	Glu	Leu	Lys
		115				120						125			
Asp	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Ser
	130					135					140				
Gln	Ala	Tyr	Leu	Gln	Gln	Ser	Gly	Ala	Glu	Leu	Val	Arg	Pro	Gly	Ala
145				150					155					160	
Ser	Val	Lys	Met	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Thr	Ser	Tyr
			165						170					175	
Asn	Met	His	Trp	Val	Lys	Gln	Thr	Pro	Arg	Gln	Gly	Leu	Glu	Trp	Ile
		180						185					190		
Gly	Ala	Ile	Tyr	Pro	Gly	Asn	Gly	Asp	Thr	Ser	Tyr	Asn	Gln	Lys	Phe
		195				200						205			
Lys	Gly	Lys	Ala	Thr	Leu	Thr	Val	Asp	Lys	Ser	Ser	Ser	Thr	Ala	Tyr
	210					215					220				
Met	Gln	Leu	Ser	Ser	Leu	Thr	Ser	Glu	Asp	Ser	Ala	Val	Tyr	Phe	Cys
225				230					235					240	
Ala	Arg	Val	Val	Tyr	Ser	Asn	Ser	Tyr	Trp	Tyr	Phe	Asp	Val	Trp	
			245					250					255		
Gly	Thr	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser	Asp	Gln	Glu	Pro	Lys	Ser
			260					265					270		
Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu
		275				280						285			
Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu
	290					295					300				
Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser
305					310				315					320	
His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu
			325					330					335		
Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr
			340					345					350		

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
355 360 365
Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
370 375 380
Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
385 390 395 400
Val Tyr Thr Leu Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
405 410 415
Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
420 425 430
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
435 440 445
Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
450 455 460
Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
465 470 475 480
Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
485 490 495
Ser Pro Gly Lys
500

<210> 241
<211> 162
<212> DNA
<213> Artificial Sequence

<220>
<223> fusion polynucleotide

<400> 241
gcggatcctt cgaacctgct cccatcctgg gccattacct taatctcagt aaatggaatt 60
tttgtgatat gctgcctgac ctactgcttt gccccaagat gcagagagag aaggaggaat 120
gagagattga gaagggaag tgtacgcct gtataaatcg at 162

<210> 242
<211> 51
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion polypeptide

<400> 242
Ala Asp Pro Ser Asn Leu Leu Pro Ser Trp Ala Ile Thr Leu Ile Ser
1 5 10 15
Val Asn Gly Ile Phe Val Ile Cys Cys Leu Thr Tyr Cys Phe Ala Pro
20 25 30
Arg Cys Arg Glu Arg Arg Arg Asn Glu Arg Leu Arg Arg Glu Ser Val
35 40 45
Arg Pro Val
50

<210> 243
<211> 399
<212> DNA
<213> Artificial Sequence

<220>
<223> fusion polynucleotide

<400> 243
aagcttatgg attttcaagt gcagattttc agcttcctgc taatcagtgcc ttcagtcata 60
atgtccagag gagtgcacat tgttctgact cagctctccag ccacctgtc tgtgactcca 120
ggagatagag tctctctttc ctgcagggcc agccagagta ttagcgacta cttacactgg 180
tatcaacaaa aatcacatga gtctccaagg ctctcatca aatatgttc ccattccatc 240
tctgggatcc cctccagggt cagtggcagt ggatcagggt cagatttcac tctcagtatc 300
aacagtgtgg aacctgaaga tgttggaatt tattactgtc aacatggtca cagctttccg 360

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
tggacgttcg gtggaggcac caagctggaa atcaaacgg 399

<210> 244
<211> 131
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion polypeptide

<400> 244
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
1 5 10 15
Val Ile Met Ser Arg Gly Val Asp Ile Val Leu Thr Gln Ser Pro Ala
20 25 30
Thr Leu Ser Val Thr Pro Gly Asp Arg Val Ser Leu Ser Cys Arg Ala
35 40 45
Ser Gln Ser Ile Ser Asp Tyr Leu His Trp Tyr Gln Gln Lys Ser His
50 55 60
Glu Ser Pro Arg Leu Leu Ile Lys Tyr Ala Ser His Ser Ile Ser Gly
65 70 75 80
Ile Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Ser Asp Phe Thr Leu
85 90 95
Ser Ile Asn Ser Val Glu Pro Glu Asp Val Gly Ile Tyr Tyr Cys Gln
100 105 110
His Gly His Ser Phe Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu
115 120 125
Ile Lys Arg
130

<210> 245
<211> 368
<212> DNA
<213> Artificial Sequence

<220>
<223> fusion polynucleotide

<400> 245
cagatccagt tgggtgcaatc tggacctgag ctgaagaagc ctggagagac agtcaggatc 60
tcttgcaagg cttctgggta tgccttcaca actactggaa tgcagtgggt gcaagagatg 120
ccaggaaagg gtttgaagtg gattggctgg ataaacaccc cactctggag tgccaaaata 180
tgtagaagac ttcaaggacg gtttgccctc tctttggaaa cctctgcaa cactgcatat 240
ttacagataa gcaacctcaa agatgaggac acggctacgt atttctgtgt gagatccggg 300
aatggtaact atgacctggc ctactttgct tactggggcc aaggagacact ggtcactgtc 360
tctgatca 368

<210> 246
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion polypeptide

<400> 246
Gln Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys Pro Gly Glu
1 5 10 15
Thr Val Arg Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Thr
20 25 30
Gly Met Gln Trp Val Gln Glu Met Pro Gly Lys Gly Leu Lys Trp Ile
35 40 45
Gly Trp Ile Asn Thr Pro Leu Trp Ser Ala Lys Ile Cys Arg Arg Leu
50 55 60
Gln Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Asn Thr Ala Tyr
65 70 75 80
Leu Gln Ile Ser Asn Leu Lys Asp Glu Asp Thr Ala Thr Tyr Phe Cys
85 90 95

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
Val Arg Ser Gly Asn Gly Asn Tyr Asp Leu Ala Tyr Phe Ala Tyr Trp
100 105 110
Gly Gln Gly Thr Leu Val Thr Val Ser
115 120

<210> 247
<211> 812
<212> DNA
<213> Artificial Sequence

<220>
<223> fusion polynucleotide

<400> 247
aagcttatgg attttcaagt gcagattttc agcttcctgc taatcagtgc ttcagtcata 60
atgtccagag gagtcgacat tgttctgact cagtctccag ccaccctgtc tgtgactcca 120
ggagatagag tctctctttc ctgcagggcc agccagagta ttagcgacta cttacactgg 180
tatcaacaaa aatcacatga gtctccaagg ctctcatca aatatgcttc ccattccatc 240
tctgggatcc cctccagggt cagtggcagt ggatcagggt cagatttcac tctcagtatc 300
aacagtgtgg aacctaaga tgggtgaatt tattactgtc aacatgggtc cagctttccg 360
tggacgttcg gtggaggcac caagctggaa atcaaacggg gtggcgggtg ctcgggcgga 420
ggtgggtcgg gtggcggcgg atctcagatc cagttgggtc aatctggacc tgagctgaag 480
aagcctggag agacagtcag gatctcctgc aaggcttctg ggtatgcctt cacaactact 540
ggaatgcagt ggggtcaaga gatgccagga aagggtttga agtggattgg ctggataaac 600
acccactct ggagtgccaa aatatgtaga agacttcaag gacggtttgc cttctctttg 660
gaaacctctg ccaacactgc atatttacag ataagcaacc tcaaagatga ggacacggct 720
acgtatttct gtgtgagatc cggaatgggt aactatgacc tggcctactt tgcttactgg 780
ggccaaggga cactggtcac tgtctctgat ca 812

<210> 248
<211> 267
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion polypeptide

<400> 248
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
1 5 10 15
Val Ile Met Ser Arg Gly Val Asp Ile Val Leu Thr Gln Ser Pro Ala
20 25 30
Thr Leu Ser Val Thr Pro Gly Asp Arg Val Ser Leu Ser Cys Arg Ala
35 40 45
Ser Gln Ser Ile Ser Asp Tyr Leu His Trp Tyr Gln Gln Lys Ser His
50 55 60
Glu Ser Pro Arg Leu Leu Ile Lys Tyr Ala Ser His Ser Ile Ser Gly
65 70 75 80
Ile Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Ser Asp Phe Thr Leu
85 90 95
Ser Ile Asn Ser Val Glu Pro Glu Asp Val Gly Ile Tyr Tyr Cys Gln
100 105 110
His Gly His Ser Phe Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu
115 120 125
Ile Lys Arg Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
130 135 140
Gly Ser Gln Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys Pro
145 150 155
Gly Glu Thr Val Arg Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr
160 165 170 175
Thr Thr Gly Met Gln Trp Val Gln Glu Met Pro Gly Lys Gly Leu Lys
180 185 190
Trp Ile Gly Trp Ile Asn Thr Pro Leu Trp Ser Ala Lys Ile Cys Arg
195 200 205
Arg Leu Gln Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Asn Thr
210 215 220
Ala Tyr Leu Gln Ile Ser Asn Leu Lys Asp Glu Asp Thr Ala Thr Tyr
225 230 235 240

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
Phe Cys Val Arg Ser Gly Asn Gly Asn Tyr Asp Leu Ala Tyr Phe Ala
245 250 255
Tyr Trp Gly Gln Gly Thr Leu Val Thr Val ser
260 265

<210> 249
<211> 405
<212> DNA
<213> Artificial Sequence

<220>
<223> fusion polynucleotide

<400> 249
atggattttc aagtcagat tttcagcttc ctgctaataca gtgcttcagt cataatgtcc 60
agaggagtcg acattgtgct cacccaatct ccagcttctt tggctgtgtc tctagggtcag 120
agagccacca tctcctgcag agccagtgaag agtggtgaat attatgtcac aagtttaatg 180
cagtgggtacc aacagaaacc aggacagcca cccaaactcc tcactctctgc tgcattccaac 240
gtagaatctg ggggtccctgc cagggttagt ggcagtgggt ctgggacaga cttcagcctc 300
aacatccatc ctgtggagga ggatgatatt gcaatgtatt tctgtcagca aagtaggaag 360
gttccttggg cggtcgggtg aggcaccaag ctggaataca aacgg 405

<210> 250
<211> 135
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion polypeptide

<400> 250
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
1 5 10 15
Val Ile Met Ser Arg Gly Val Asp Ile Val Leu Thr Gln Ser Pro Ala
20 25 30
Ser Leu Ala Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys Arg Ala
35 40 45
Ser Glu Ser Val Glu Tyr Tyr Val Thr Ser Leu Met Gln Trp Tyr Gln
50 55 60
Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Ser Ala Ala Ser Asn
65 70 75 80
Val Glu Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Thr
85 90 95
Asp Phe Ser Leu Asn Ile His Pro Val Glu Glu Asp Asp Ile Ala Met
100 105 110
Tyr Phe Cys Gln Gln Ser Arg Lys Val Pro Trp Thr Phe Gly Gly Gly
115 120 125
Thr Lys Leu Glu Ile Lys Arg
130 135

<210> 251
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<223> fusion polynucleotide

<400> 251
cagggtcagc tgaaggagtc aggacctggc ctggtggcgc cctcacagag cctgtccatc 60
acatgcaccg tctcagggtt ctcattaacc ggctatgggt taaactgggt tcgccagcct 120
ccaggaaagg gtctggagtg gctgggaatg atatgggggt atggaagcac agactataat 180
tcagctctca aatccagact gagcatcacc aaggacaact ccaagagcca agttttctta 240
aaaatgaaca gtctgcaaac tgatgacaca gccagatact actgtgccag agatggttat 300
agtaactttc attactatgt tatggactac tgggggtcaag gaacctcagt caccgtctcc 360
tcagatctg 369

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt

<210> 252
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion polypeptide

<400> 252
Gln Val Gln Leu Lys Glu Ser Gly Pro Gly Leu Val Ala Pro Ser Gln
1 5 10 15
Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Gly Tyr
20 25 30
Gly Val Asn Trp Val Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Leu
35 40 45
Gly Met Ile Trp Gly Asp Gly Ser Thr Asp Tyr Asn Ser Ala Leu Lys
50 55 60
Ser Arg Leu Ser Ile Thr Lys Asp Asn Ser Lys Ser Gln Val Phe Leu
65 70 75 80
Lys Met Asn Ser Leu Gln Thr Asp Asp Thr Ala Arg Tyr Tyr Cys Ala
85 90 95
Arg Asp Gly Tyr Ser Asn Phe His Tyr Tyr Val Met Asp Tyr Trp Gly
100 105 110
Gln Gly Thr Ser Val Thr Val Ser Ser
115 120

<210> 253
<211> 825
<212> DNA
<213> Artificial Sequence

<220>
<223> fusion polynucleotide

<400> 253
aagcttatgg attttcaagt gcagattttc agcttcctgc taatcagtgc ttcagtcata 60
atgtccagag gagtgcgacat tgtgctcacc caatctccag cttctttggc tgtgtctcta 120
ggtcagagag ccaccatctc ctgcagagcc agtgaaagtg ttgaatatta tgtcacaagt 180
ttaatgcagt ggtaccaaca gaaaccagga cagccaccca aactcctcat ctctgctgca 240
tccaacgtag aatctggggg cctgccagg tttagtggca gtgggtctgg gacagacttc 300
agcctcaaca tccatcctgt ggaggaggat gatattgcaa tgtatttctg tcagcaaagt 360
aggaagggtc cttggacgtt cgggtggaggc accaagctgg aaatcaaacg ggggtggcgg 420
ggctcgggcg gagggtgggtc ggggtggcggc ggatctcagg tgcagctgaa ggagtcagga 480
cctggcctgg tggcgccctc acagagcctg tccatcacat gcaccgtctc agggttctca 540
ttaaccggct atggtgtaaa ctgggttcgc cagcctccag gaaaggggtc ggagtggctg 600
ggaatgatat ggggtgatgg aagcacagac tataattcag ctctcaaadc cagactgagc 660
atcaccaagg acaactccaa gagccaagtt ttcttaaaaa tgaacagtct gcaactgat 720
gacacagcca gatactactg tgccagagat ggttatagta actttcatta ctatgttatg 780
gactactggg gtcaaggaac ctcagtcacc gtctcctctg atcag 825

<210> 254
<211> 271
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion polypeptide

<400> 254
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
1 5 10 15
Val Ile Met Ser Arg Gly Val Asp Ile Val Leu Thr Gln Ser Pro Ala
20 25 30
Ser Leu Ala Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys Arg Ala
35 40 45
Ser Glu Ser Val Glu Tyr Tyr Val Thr Ser Leu Met Gln Trp Tyr Gln
50 55 60
Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Ser Ala Ala Ser Asn

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65	Val	Glu	Ser	Gly	Val	Pro	Ala	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	80
				85						90						95	
	Asp	Phe	Ser	Leu	Asn	Ile	His	Pro	Val	Glu	Glu	Asp	Asp	Ile	Ala	Met	
				100					105					110			
	Tyr	Phe	Cys	Gln	Gln	Ser	Arg	Lys	Val	Pro	Trp	Thr	Phe	Gly	Gly	Gly	
			115					120					125				
	Thr	Lys	Leu	Glu	Ile	Lys	Arg	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	
			130				135					140					
	Ser	Gly	Gly	Gly	Gly	Ser	Gln	Val	Gln	Leu	Lys	Glu	Ser	Gly	Pro	Gly	
			145			150					155					160	
	Leu	Val	Ala	Pro	Ser	Gln	Ser	Leu	Ser	Ile	Thr	Cys	Thr	Val	Ser	Gly	
				165						170					175		
	Phe	Ser	Leu	Thr	Gly	Tyr	Gly	Val	Asn	Trp	Val	Arg	Gln	Pro	Pro	Gly	
			180						185					190			
	Lys	Gly	Leu	Glu	Trp	Leu	Gly	Met	Ile	Trp	Gly	Asp	Gly	Ser	Thr	Asp	
			195				200						205				
	Tyr	Asn	Ser	Ala	Leu	Lys	Ser	Arg	Leu	Ser	Ile	Thr	Lys	Asp	Asn	Ser	
			210			215						220					
	Lys	Ser	Gln	Val	Phe	Leu	Lys	Met	Asn	Ser	Leu	Gln	Thr	Asp	Asp	Thr	
			225			230					235					240	
	Ala	Arg	Tyr	Tyr	Cys	Ala	Arg	Asp	Gly	Tyr	Ser	Asn	Phe	His	Tyr	Tyr	
				245						250					255		
	Val	Met	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Ser	Val	Thr	Val	Ser	Ser		
			260						265					270			

<210> 255
<211> 393
<212> DNA
<213> Artificial Sequence

<220>
<223> fusion polynucleotide

<400> 255
atggattttc aagtgcagat tttcagcttc ctgctaataca gtgcttcagt cataatgtcc 60
agaggagtcg acatccagat gacacagtct ccatcctcac tgtctgcatc tctgggaggc 120
aaagtcacca tcacttgcaa ggcaagccaa gacattaaga agtatatagg ttgggtaccaa 180
cacaagcctg gaaaaggctc caggctgtct atatattaca catctacatt acagccaggc 240
atcccatcaa ggttcagtgg aagtgggtct gggagagatt attccctcag catcagaaac 300
ctggagcctg aagatattgc aacttattat tgtcaacagt atgataatct tccattgacg 360
ttcggctcgg ggacaaagtt ggaaataaaa cgg 393

<210> 256
<211> 131
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion polypeptide

<400> 256
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
1 5 10 15
Val Ile Met Ser Arg Gly Val Asp Ile Gln Met Thr Gln Ser Pro Ser
20 25 30
Ser Leu Ser Ala Ser Leu Gly Gly Lys Val Thr Ile Thr Cys Lys Ala
35 40 45
Ser Gln Asp Ile Lys Lys Tyr Ile Gly Trp Tyr Gln His Lys Pro Gly
50 55 60
Lys Gly Pro Arg Leu Leu Ile Tyr Tyr Thr Ser Thr Leu Gln Pro Gly
65 70 75 80
Ile Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Arg Asp Tyr Ser Leu
85 90 95
Ser Ile Arg Asn Leu Glu Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln
100 105 110
Gln Tyr Asp Asn Leu Pro Leu Thr Phe Gly Ser Gly Thr Lys Leu Glu
115 120 125

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
Ile Lys Arg
130

<210> 257
<211> 362
<212> DNA
<213> Artificial Sequence

<220>
<223> fusion polynucleotide

<400> 257
gatgtacagc ttcaggagtc aggacctggc ctcgtgaaac cttctcagtc tctgtctctc 60
acctgctctg tcaactggcta ctccatcacc agtggtttct actggaactg gatccgacag 120
tttccgggaa acaaaactgga atggatgggc cacataagcc acgacggtag gaataactac 180
aaccatctc tcataaatcg aatctccatc actcgtgaca catctaagaa ccagtttttc 240
ctgaagttga gttctgtgac tactgaggac acagctacat atttctgtgc aagacactac 300
ggtagtagcg gagctatgga ctactggggt caaggaacct cagtcaccgt ctctctgat 360
ca 362

<210> 258
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion polypeptide

<400> 258
Asp Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15
Ser Leu Ser Leu Thr Cys Ser Val Thr Gly Tyr Ser Ile Thr Ser Gly
20 25 30
Phe Tyr Trp Asn Trp Ile Arg Gln Phe Pro Gly Asn Lys Leu Glu Trp
35 40 45
Met Gly His Ile Ser His Asp Gly Arg Asn Asn Tyr Asn Pro Ser Leu
50 55 60
Ile Asn Arg Ile Ser Ile Thr Arg Asp Thr Ser Lys Asn Gln Phe Phe
65 70 75 80
Leu Lys Leu Ser Ser Val Thr Thr Glu Asp Thr Ala Thr Tyr Phe Cys
85 90 95
Ala Arg His Tyr Gly Ser Ser Gly Ala Met Asp Tyr Trp Gly Gln Gly
100 105 110
Thr Ser Val Thr Val Ser Ser
115

<210> 259
<211> 806
<212> DNA
<213> Artificial Sequence

<220>
<223> fusion polynucleotide

<400> 259
aagcttatgg attttcaagt gcagattttc agcttcctgc taatcagtg cttcagtcata 60
atgtccagag gagtcgacat ccagatgaca cagtcctcat cctcactgtc tgcattctctg 120
ggaggcaaag tcaccatcac ttgcaaggca agccaagaca ttaagaagta tataggttgg 180
taccaacaca agcctggaag aggtcccagg ctgctcatat attacacatc tacattacag 240
ccaggcatcc catcaagggt cagtgggaagt gggctctggga gagattattc cctcagcatc 300
agaaacctgg agcctgaaga tattgcaact tattattgtc aacagtatga taatcttcca 360
ttgacgttcg gctcggggac aaagtgtgaa ataaaacggg gtggcggtgg ctcgggcggt 420
ggtgggtcgg gtggcgggcg atctgatgta cagcttcagg agtcaggacc tggcctctgt 480
aaaccttctc agtctctgtc tctcacctgc tctgtcactg gctactccat caccagtggt 540
ttctactgga actggatccg acagtttccg tctctcataa ttcgaatctc catcactcgt 600
agccacgacg gtaggaataa ctacaaccca tctctcataa atcgaatctc catcactcgt 660
gacacatcta agaaccagtt tttcctgaag ttgagttctg tgactactga ggacacagct 720

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
acatatttct gtgcaagaca ctacgtagt agcggagcta tggactactg gggtaagga 780
acctcagta ccgtctcctc tgatca 806

<210> 260
<211> 266
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion polypeptide

<400> 260
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
1 5 10 15
Val Ile Met Ser Arg Gly Val Asp Ile Gln Met Thr Gln Ser Pro Ser
20 25 30
Ser Leu Ser Ala Ser Leu Gly Gly Lys Val Thr Ile Thr Cys Lys Ala
35 40 45
Ser Gln Asp Ile Lys Lys Tyr Ile Gly Trp Tyr Gln His Lys Pro Gly
50 55 60
Lys Gly Pro Arg Leu Leu Ile Tyr Tyr Thr Ser Thr Leu Gln Pro Gly
65 70 75 80
Ile Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Arg Asp Tyr Ser Leu
85 90 95
Ser Ile Arg Asn Leu Glu Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln
100 105 110
Gln Tyr Asp Asn Leu Pro Leu Thr Phe Gly Ser Gly Thr Lys Leu Glu
115 120 125
Ile Lys Arg Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
130 135 140
Gly Ser Asp Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro
145 150 155 160
Ser Gln Ser Leu Ser Leu Thr Cys Ser Val Thr Gly Tyr Ser Ile Thr
165 170 175
Ser Gly Phe Tyr Trp Asn Trp Ile Arg Gln Phe Pro Gly Asn Lys Leu
180 185 190
Glu Trp Met Gly His Ile Ser His Asp Gly Arg Asn Asn Tyr Asn Pro
195 200 205
Ser Leu Ile Asn Arg Ile Ser Ile Thr Arg Asp Thr Ser Lys Asn Gln
210 215 220
Phe Phe Leu Lys Leu Ser Ser Val Thr Thr Glu Asp Thr Ala Thr Tyr
225 230 235 240
Phe Cys Ala Arg His Tyr Gly Ser Ser Gly Ala Met Asp Tyr Trp Gly
245 250 255
Gln Gly Thr Ser Val Thr Val Ser Ser Asp
260 265

<210> 261
<211> 417
<212> DNA
<213> Artificial Sequence

<220>
<223> fusion polynucleotide

<400> 261
atggcatgga gctgcattat tttcttcttg gtatcagtaa ttacagggtg ccattcccag 60
gtcaagctgc agcagtccgg ttctgaacta gggaaacctg gggcctcagt gaaactgtcc 120
tgcaagactt caggctacat attcacagat cactatattt cttgggtgaa acagaagcct 180
ggagaaagcc tgcagtggat aggaatgtt tatggtggaa atggtgttac aagctacaat 240
caaaaattcc agggcaaggc cacactgact gtagataaaa tctctagcac agcctacatg 300
gaactcagca gcctgacatc tgaggattct gccatctatt actgtgcaag aaggccggta 360
gcgacgggcc atgctatgga ctactggggg caggggatcc aagttaccgt ctcctca 417

<210> 262
<211> 139
<212> PRT
<213> Artificial Sequence

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<220>

<223> fusion polypeptide

<400> 262

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Met Ala Trp Ser Cys Ile Ile Phe Phe Leu Val Ser Val Ile Thr Gly
 1      5      10      15
Val His Ser Gln Val Lys Leu Gln Gln Ser Gly Ser Glu Leu Gly Lys
 20      25      30
Pro Gly Ala Ser Val Lys Leu Ser Cys Lys Thr Ser Gly Tyr Ile Phe
 35      40      45
Thr Asp His Tyr Ile Ser Trp Val Lys Gln Lys Pro Gly Glu Ser Leu
 50      55      60
Gln Trp Ile Gly Asn Val Tyr Gly Gly Asn Gly Gly Thr Ser Tyr Asn
 65      70      75
Gln Lys Phe Gln Gly Lys Ala Thr Leu Thr Val Asp Lys Ile Ser Ser
 85      90      95
Thr Ala Tyr Met Glu Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Ile
100      105      110
Tyr Tyr Cys Ala Arg Arg Pro Val Ala Thr Gly His Ala Met Asp Tyr
115      120      125
Trp Gly Gln Gly Ile Gln Val Thr Val Ser Ser
130      135

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<210> 263

<211> 381

<212> DNA

<213> Artificial Sequence

<220>

<223> fusion polynucleotide

<400> 263

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atgttggtata catctcagct ccttgggctt ttactcttct ggatttcagc ctccagaagt 60
gacatagtgc tgactcagac tccagccact ctgtctctaa ttccctggaga aagagtcaca 120
atgacctgta agaccagtca gaattattggc acaatcttac actggtatca ccaaaaacca 180
aaggaggctc caagggtctt catcaagtat gcttcgcagt ccattcctgg gatccctcc 240
agattcagtg gcagtgggtc ggaaacagat ttcactctca gcatcaataa cctggagcct 300
gatgatatcg gaatttatta ctgtcaacaa agtagaagct ggctgtcac gttcggctct 360
ggcaccaagc tggagataaa a
381

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<210> 264

<211> 127

<212> PRT

<213> Artificial Sequence

<220>

<223> fusion polypeptide

<400> 264

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Met Leu Tyr Thr Ser Gln Leu Leu Gly Leu Leu Leu Phe Trp Ile Ser
 1      5      10      15
Ala Ser Arg Ser Asp Ile Val Leu Thr Gln Thr Pro Ala Thr Leu Ser
 20      25      30
Leu Ile Pro Gly Glu Arg Val Thr Met Thr Cys Lys Thr Ser Gln Asn
 35      40      45
Ile Gly Thr Ile Leu His Trp Tyr His Gln Lys Pro Lys Glu Ala Pro
 50      55      60
Arg Ala Leu Ile Lys Tyr Ala Ser Gln Ser Ile Pro Gly Ile Pro Ser
 65      70      75
Arg Phe Ser Gly Ser Gly Ser Glu Thr Asp Phe Thr Leu Ser Ile Asn
 85      90      95
Asn Leu Glu Pro Asp Asp Ile Gly Ile Tyr Tyr Cys Gln Gln Ser Arg
100      105      110
Ser Trp Pro Val Thr Phe Gly Pro Gly Thr Lys Leu Glu Ile Lys
115      120      125

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<210> 265
<211> 1671
<212> DNA
<213> Artificial Sequence

<220>
<223> fusion polynucleotide

<400> 265
aagcttatgg attttcaagt gcagattttc agcttcctgc taatcagtgc ttcagtcata 60
atgtccagag gagtcgacat tgttctgact cagttctccag ccaccctgtc tgtgactcca 120
ggagatagag tctctctttc ctgcagggcc agccagagta ttagcgacta cttacactgg 180
tatcaacaaa aatcacatga gtctccaagg cttctcatca aatatgtctc ccattccatc 240
tctgggatcc cctccagggt cagtggcagt ggatcagggt cagatttcac tctcagtatc 300
aacagtgtgg aacctgaaga tgttggaaatt tattactgtc aacatgggtc cagctttccg 360
tggagcttcg gtggaggcac caagctggaa atcaaacggg gtggcggtgg ctccggcgga 420
ggtgggtcgg gtggcggtcg atctcagatc cagttgggtc aatctggacc tgagctgaag 480
aagcctggag agacagtcag gatctcctgc aaggcttctg ggtatgcctt cacaactact 540
ggaatgcagt ggtgtcaaga gatgccagga aagggtttga agtggattgg ctggataaac 600
acccactctt ggagtgccaa aatatgtaga agacttcaag gacggtttgc cttctctttg 660
gaaacctctg ccaacactgc atattttacag ataagcaacc tcaaagatga ggacacggct 720
acgtatttct gtgtgagatc cggaatggtt aactatgacc tggcctactt tgcttactgg 780
ggccaaggga cactgggtcac tgtctctgat ctggagccca aatcttctga caaaactcac 840
acatccccac cgtccccagc acctgaactc ctggggggat cgtcagtctt cctcttcccc 900
ccaaaaccca aggacaccct catgatctcc cggacccttg aggtcacatg cgtgggtggtg 960
gacgtgagcc acgaagaccc tgaggtcaag ttcaactggt acgtggacgg cgtggagggtg 1020
cataatgccca agacaaagcc gcgggaggag cagtacaaca gcacgtaccg tgtggctcagc 1080
gtcctcaccg tcttgaccca ggactggctg aatggcaagg agtacaagtg caaggctctc 1140
aacaagagccc tcccagcccc catcgagaaa accatctcca aagccaaagg gcagccccga 1200
gaaccacagg tgtaaccctt gccccatccc cgggatgagc tgaccaagaa ccaggtcagc 1260
ctgacgtgcc tgggtcaaagg cttctatccc agcgacatcg ccgtggagtg ggagagcaat 1320
gggcagccgg agaacaacta caagaccacg cctcccgtgc tggactccga cggctccttc 1380
ttcctctaca gcaagctcac cgtggacaag agcaggtggc agcaggggaa cgtcttctca 1440
tgtctcgtga tgcattgaggc tctgcacaac cactacacgc agaagagcct ctccctgtct 1500
ccgggtaaaag cggatccttc gaacctgctc ccatctggg ccattacctt aatctcagta 1560
aatggaattt ttgtgatatg ctgcctgacc tactgctttg cccaagatg cagagagaga 1620
aggaggaatg agagattgag aagggaaagt gtacgccttg tataaatcga t 1671

<210> 266
<211> 552
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion polypeptide

<400> 266
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
1 5 10 15
Val Ile Met Ser Arg Gly Val Asp Ile Val Leu Thr Gln Ser Pro Ala
20 25 30
Thr Leu Ser Val Thr Pro Gly Asp Arg Val Ser Leu Ser Cys Arg Ala
35 40 45
Ser Gln Ser Ile Ser Asp Tyr Leu His Trp Tyr Gln Gln Lys Ser His
50 55 60
Glu Ser Pro Arg Leu Leu Ile Lys Tyr Ala Ser His Ser Ile Ser Gly
65 70 75 80
Ile Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Ser Asp Phe Thr Leu
85 90 95
Ser Ile Asn Ser Val Glu Pro Glu Asp Val Gly Ile Tyr Tyr Cys Gln
100 105 110
His Gly His Ser Phe Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu
115 120 125
Ile Lys Arg Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
130 135 140
Gly Ser Gln Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys Pro
145 150 155 160
Gly Glu Thr Val Arg Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr
165 170 175

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 Thr Thr Gly Met Gln Trp Val Gln Glu Met Pro Gly Lys Gly Leu Lys
 180 185 190
 Trp Ile Gly Trp Ile Asn Thr Pro Leu Trp Ser Ala Lys Ile Cys Arg
 195 200 205
 Arg Leu Gln Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Asn Thr
 210 215 220
 Ala Tyr Leu Gln Ile Ser Asn Leu Lys Asp Glu Asp Thr Ala Thr Tyr
 225 230 235 240
 Phe Cys Val Arg Ser Gly Asn Gly Asn Tyr Asp Leu Ala Tyr Phe Ala
 245 250 255
 Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Asp Leu Glu Pro Lys
 260 265 270
 Ser Ser Asp Lys Thr His Thr Ser Pro Pro Ser Pro Ala Pro Glu Leu
 275 280 285
 Leu Gly Gly Ser Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
 290 295 300
 Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
 305 310 315 320
 Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
 325 330 335
 Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
 340 345 350
 Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
 355 360 365
 Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
 370 375 380
 Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
 385 390 395 400
 Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln
 405 410 415
 Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
 420 425 430
 Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
 435 440 445
 Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
 450 455 460
 Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
 465 470 475 480
 Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
 485 490 495
 Leu Ser Pro Gly Lys Ala Asp Pro Ser Asn Leu Leu Pro Ser Trp Ala
 500 505 510
 Ile Thr Leu Ile Ser Val Asn Gly Ile Phe Val Ile Cys Cys Leu Thr
 515 520 525
 Tyr Cys Phe Ala Pro Arg Cys Arg Glu Arg Arg Arg Asn Glu Arg Leu
 530 535 540
 Arg Arg Glu Ser Val Arg Pro Val
 545 550

<210> 267
 <211> 1683
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> fusion polynucleotide

<400> 267
 aagcttatgg attttcaagt gcagattttc agcttcctgc taatcagtg ttcagtcata 60
 atgtccagag gagtcgacat tgtgctcacc caatctccag cttctttggc tgtgtctcta 120
 ggtcagagag ccaccatctc ctgcagagcc agtgaaagtg ttgaatatta tgtcacaagt 180
 ttaatgcagt ggtaccaaca gaaaccagga cagccaccca aactcctcat ctctgctgca 240
 tccaacgtag aatctggggg ccctgccagg ttttagtgga gtgggtctgg gacagacttc 300
 agcctcaaca tccatcctgt ggaggaggat gatattgcaa tgtatttctg tcagcaaagt 360
 aggaagggtt cttggacgtt cggtggaggg accaagctgg aaatcaaacg ggggtggcgg 420
 ggctcggggc gaggtgggtc ggggtggcgg gcattctcagg tgcagctgaa ggagtcagga 480
 cctggcctgg tggcgccctc acagagcctg tccatcacat gcaccgtctc agggttctca 540
 ttaaccggct atggtgtaaa ctgggttcgc cagcctccag gaaaggggtc ggagtggctg 600

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
 ggaatgatata ggggtgatgg aagcacagac tataattcag ctctcaaatac cagactgagc 660
 atcaccaagg acaactccaa gagccaagtt ttcttaaaaa tgaacagtct gcaaaactgat 720
 gacacagcca gataactactg tgccagagat ggttatagta actttcatta ctatgttatg 780
 gactactggg gtcaaggaac ctgagtcacc gtctcctcag atctggagcc caaatcttct 840
 gacaaaactc acacatcccc accgtcccca gcacctgaac tcctgggggg atcgtcagtc 900
 ttctcttctc ccccaaaacc caaggacacc ctcatgatct cccggacccc tgaggtcaca 960
 tgcgtgggtg tggacgtgag ccacgaagac cctgaggtca agttcaactg gtacgtggac 1020
 ggcgtggagg tgcataatgc caagacaaag ccgcggggagg agcagtacaa cagcacgtac 1080
 cgtgtgggtca gcgtcctcac cgtcctgcac caggactggc tgaatggcaa ggagtacaag 1140
 tgcaagggtc ccaacaaagc cctcccagcc cccatcgaga aaaccatctc caaagccaaa 1200
 gggcagcccc gagaaccaca ggtgtacacc ctgccccat cccgggatga gctgaccaag 1260
 aaccaggtca gcctgacctg cctgggtcaaa ggcttctatc ccagcgacat gccgtggag 1320
 tgggagagca atgggcagcc ggagaacaac tacaagacca cgctcccgt gctggactcc 1380
 gacggctcct tcttctctta cagcaagctc accgtggaca agagcaggtg gcagcagggg 1440
 aacgtcttct catgctccgt gatgcatgag gctctgcaca accactacac gcagaagagc 1500
 ctctccctgt ctccgggtaa agcggatcct tcgaacctgc tcccatcctg gccattacc 1560
 ttaatctcag taaatggaat ttttgtgata tgctgcctga cctactgctt tgccccaaga 1620
 tgcagagaga gaaggaggaa tgagagattg agaagggaaa gtgtacgcc tgtataaatc 1680
 gat 1683

<210> 268
 <211> 556
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> fusion polypeptide

<400> 268
 Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1 5 10 15
 Val Ile Met Ser Arg Gly Val Asp Ile Val Leu Thr Gln Ser Pro Ala
 20 25 30
 Ser Leu Ala Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys Arg Ala
 35 40 45
 Ser Glu Ser Val Glu Tyr Tyr Val Thr Ser Leu Met Gln Trp Tyr Gln
 50 55 60
 Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Ser Ala Ala Ser Asn
 65 70 75 80
 Val Glu Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr
 85 90 95
 Asp Phe Ser Leu Asn Ile His Pro Val Glu Glu Asp Asp Ile Ala Met
 100 105 110
 Tyr Phe Cys Gln Gln Ser Arg Lys Val Pro Trp Thr Phe Gly Gly Gly
 115 120 125
 Thr Lys Leu Glu Ile Lys Arg Gly Gly Gly Ser Gly Gly Gly Gly
 130 135 140
 Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Lys Glu Ser Gly Pro Gly
 145 150 155 160
 Leu Val Ala Pro Ser Gln Ser Leu Ser Ile Thr Cys Thr Val Ser Gly
 165 170 175
 Phe Ser Leu Thr Gly Tyr Gly Val Asn Trp Val Arg Gln Pro Pro Gly
 180 185 190
 Lys Gly Leu Glu Trp Leu Gly Met Ile Trp Gly Asp Gly Ser Thr Asp
 195 200 205
 Tyr Asn Ser Ala Leu Lys Ser Arg Leu Ser Ile Thr Lys Asp Asn Ser
 210 215 220
 Lys Ser Gln Val Phe Leu Lys Met Asn Ser Leu Gln Thr Asp Asp Thr
 225 230 235 240
 Ala Arg Tyr Tyr Cys Ala Arg Asp Gly Tyr Ser Asn Phe His Tyr Tyr
 245 250 255
 Val Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Asp
 260 265 270
 Leu Glu Pro Lys Ser Ser Asp Lys Thr His Thr Ser Pro Pro Ser Pro
 275 280 285
 Ala Pro Glu Leu Leu Gly Gly Ser Ser Val Phe Leu Phe Pro Pro Lys
 290 295 300
 Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
 305 310 315 320

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Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
325 330 335
Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
340 345 350
Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
355 360 365
Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
370 375 380
Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
385 390 395 400
Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
405 410 415
Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
420 425 430
Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
435 440 445
Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
450 455 460
Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
465 470 475 480
Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
485 490 495
Lys Ser Leu Ser Leu Ser Pro Gly Lys Ala Asp Pro Ser Asn Leu Leu
500 505 510
Pro Ser Trp Ala Ile Thr Leu Ile Ser Val Asn Gly Ile Phe Val Ile
515 520 525
Cys Cys Leu Thr Tyr Cys Phe Ala Pro Arg Cys Arg Glu Arg Arg Arg
530 535 540
Asn Glu Arg Leu Arg Arg Glu Ser Val Arg Pro Val
545 550 555

<210> 269
<211> 1665
<212> DNA
<213> Artificial sequence

<220>
<223> fusion polynucleotide

<400> 269
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ggaggcaaaag tcaccatcac ttgcaaggca agccaagaca ttaagaagta tataggttgg 180
taccaacaca agcctggaaa aggtcccagg ctgctcatat attacacatc tacattacag 240
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agaaacctgg agcctgaaga tattgcaact tattattgtc aacagtatga taatcttcca 360
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gggtgggtcgg gtggcgggcg atctgatgta cagcttcagg agtcaggacc tggcctcgtg 480
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ttctactgga actggatccg acagtttccg ggaaacaaac tgggaatggat gggccacata 600
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caggtgtaca ccctgcccc atcccgggat gagctgacca agaaccaggt cagcctgacc 1260
tgcttggtca aaggcttcta tcccagcgac atcgccgtgg agtgggagag caatgggcag 1320
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atttttgtga tatgctgcct gacctactgc ttggcccaa gatgcagaga gagaaggagg 1620
aatgagagat tgagaaggga aagtgtacgc cctgtataaa tcgat 1665

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<210> 270
<211> 550
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion polypeptide

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Ser Leu Ser Ala Ser Leu Gly Gly Lys Val Thr Ile Thr Cys Lys Ala
35 40 45
Ser Gln Asp Ile Lys Lys Tyr Ile Gly Trp Tyr Gln His Lys Pro Gly
50 55 60
Lys Gly Pro Arg Leu Leu Ile Tyr Tyr Thr Ser Thr Leu Gln Pro Gly
65 70 75 80
Ile Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Arg Asp Tyr Ser Leu
85 90 95
Ser Ile Arg Asn Leu Glu Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln
100 105 110
Gln Tyr Asp Asn Leu Pro Leu Thr Phe Gly Ser Gly Thr Lys Leu Glu
115 120 125
Ile Lys Arg Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
130 135 140
Gly Ser Asp Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro
145 150 155 160
Ser Gln Ser Leu Ser Leu Thr Cys Ser Val Thr Gly Tyr Ser Ile Thr
165 170 175
Ser Gly Phe Tyr Trp Asn Trp Ile Arg Gln Phe Pro Gly Asn Lys Leu
180 185 190
Glu Trp Met Gly His Ile Ser His Asp Gly Arg Asn Asn Tyr Asn Pro
195 200 205
Ser Leu Ile Asn Arg Ile Ser Ile Thr Arg Asp Thr Ser Lys Asn Gln
210 215 220
Phe Phe Leu Lys Leu Ser Ser Val Thr Thr Glu Asp Thr Ala Thr Tyr
225 230 235 240
Phe Cys Ala Arg His Tyr Gly Ser Ser Gly Ala Met Asp Tyr Trp Gly
245 250 255
Gln Gly Thr Ser Val Thr Val Ser Ser Asp Leu Glu Pro Lys Ser Ser
260 265 270
Asp Lys Thr His Thr Ser Pro Pro Ser Pro Ala Pro Glu Leu Leu Gly
275 280 285
Gly Ser Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
290 295 300
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
305 310 315 320
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
325 330 335
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
340 345 350
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
355 360 365
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
370 375 380
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
385 390 395 400
Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
405 410 415
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
420 425 430
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
435 440 445
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
450 455 460
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
 465 470 475 480
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 485 490 495
 Pro Gly Lys Ala Asp Pro Ser Asn Leu Leu Pro Ser Trp Ala Ile Thr
 500 505 510
 Leu Ile Ser Val Asn Gly Ile Phe Val Ile Cys Cys Leu Thr Tyr Cys
 515 520 525
 Phe Ala Pro Arg Cys Arg Glu Arg Arg Arg Asn Glu Arg Leu Arg Arg
 530 535 540
 Glu Ser Val Arg Pro Val
 545 550

<210> 271
 <211> 1653
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> fusion polynucleotide

<400> 271
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 atgacctgta agaccagtca gaattattggc acaatcttac actggtatca ccaaaaacca 180
 aaggaggctc caagggtctt catcaagtat gcttcgcagt ccattcctgg gatccccctc 240
 agattcagtg gcagtgggtt ggaaacagat ttactctca gcatcaataa cctggagcct 300
 gatgatatcg gaatttatta ctgtcaacaa agtagaagct ggctgtcac gttcggctcct 360
 ggaccaagc tggagataaa acgggggtggc ggtggctcgg gcggaggtgg gtcgggtggc 420
 ggcggtatct aggtcaagct gcagcagtc gggtctgaac tagggaaacc tggggcctca 480
 gtgaaactgt cctgcaagac ttcaggctac atattcacag atcactatat ttcttgggtg 540
 aacagaagc ctggagaaag cctgcagtgg ataggaaatg ttatgggtg aaatgggtgg 600
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 cctgaggtca agttcaactg gtacgtggac ggcgtggagg tgcataatgc caagacaaag 1020
 ccgcgggagg agcagtacaa cagcacgtac cgtgtggtca gcgtcctcac cgtcctgcac 1080
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 ctgcccccat cccgggatga gctgaccaag aaccagggtc gcctgacctg cctggtcaaa 1260
 ggcttctatc ccagcgacat cgccgtggag tgggagagca atggggcagc ggagaacaac 1320
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 tcgaacctgc tcccactctg ggccattacc ttaatctcag taaatggaat tttgtgata 1560
 tgctgcctga cctactgctt tgccccaaga tgcagagaga gaaggaggaa tgagagattg 1620
 agaagggaaa gtgtacgcc tgtataaatc gat 1653

<210> 272
 <211> 548
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> fusion polypeptide

<400> 272
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 20 25 30
 Leu Ile Pro Gly Glu Arg Val Thr Met Thr Cys Lys Thr Ser Gln Asn
 35 40 45
 Ile Gly Thr Ile Leu His Trp Tyr His Gln Lys Pro Lys Glu Ala Pro
 50 55 60
 Arg Ala Leu Ile Lys Tyr Ala Ser Gln Ser Ile Pro Gly Ile Pro Ser

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
 65 70 75 80
 Arg Phe Ser Gly Ser Gly Ser Glu Thr Asp Phe Thr Leu Ser Ile Asn
 85 90 95
 Asn Leu Glu Pro Asp Asp Ile Gly Ile Tyr Tyr Cys Gln Gln Ser Arg
 100 105 110
 Ser Trp Pro Val Thr Phe Gly Pro Gly Thr Lys Leu Glu Ile Lys Arg
 115 120 125
 Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln
 130 135 140
 Val Lys Leu Gln Gln Ser Gly Ser Glu Leu Gly Lys Pro Gly Ala Ser
 145 150 155 160
 Val Lys Leu Ser Cys Lys Thr Ser Gly Tyr Ile Phe Thr Asp His Tyr
 165 170 175
 Ile Ser Trp Val Lys Gln Lys Pro Gly Glu Ser Leu Gln Trp Ile Gly
 180 185 190
 Asn Val Tyr Gly Gly Asn Gly Gly Thr Ser Tyr Asn Gln Lys Phe Gln
 195 200 205
 Gly Lys Ala Thr Leu Thr Val Asp Lys Ile Ser Ser Thr Ala Tyr Met
 210 215 220
 Glu Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Ile Tyr Tyr Cys Ala
 225 230 235 240
 Arg Arg Pro Val Ala Thr Gly His Ala Met Asp Tyr Trp Gly Gln Gly
 245 250 255
 Ile Gln Val Thr Val Ser Ser Asp Leu Glu Pro Lys Ser Ser Asp Lys
 260 265 270
 Thr His Thr Ser Pro Pro Ser Pro Ala Pro Glu Leu Leu Gly Gly Ser
 275 280 285
 Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
 290 295 300
 Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
 305 310 315 320
 Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
 325 330 335
 Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
 340 345 350
 Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
 355 360 365
 Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
 370 375 380
 Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
 385 390 395 400
 Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
 405 410 415
 Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
 420 425 430
 Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Val Leu
 435 440 445
 Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
 450 455 460
 Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
 465 470 475 480
 Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
 485 490 495
 Lys Ala Asp Pro Ser Asn Leu Leu Pro Ser Trp Ala Ile Thr Leu Ile
 500 505 510
 Ser Val Asn Gly Ile Phe Val Ile Cys Cys Leu Thr Tyr Cys Phe Ala
 515 520 525
 Pro Arg Cys Arg Glu Arg Arg Asn Glu Arg Leu Arg Arg Glu Ser
 530 535 540
 Val Arg Pro Val
 545

<210> 273
 <211> 1521
 <212> DNA
 <213> Artificial sequence
 <220>

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
<223> fusion polynucleotide

<400> 273

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1521

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<210> 274

<211> 500

<212> PRT

<213> Artificial Sequence

<220>

<223> fusion polypeptide

<400> 274

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Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser
35     40     45
Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser
50     55     60
Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro
65     70     75     80
Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
85     90     95
Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
100    105    110
Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
115    120    125
Asp Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Ser
130    135    140
Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala
145    150    155    160
Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
165    170    175
Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile
180    185    190
Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
195    200    205
Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Thr Ala Tyr
210    215    220
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
225    230    235    240

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<400> 277
gttggtgatc aggagcccaa atctgtgac aaaactcac 39

<210> 278
<211> 52
<212> DNA
<213> Artificial Sequence

<220>
<223> 3' oligo to amplify constant regions for creating
      IgG hinge mutants

<400> 278
gttggttcta gatcatttac ccggagacag ggagaggctc ttctgctgt ag 52

<210> 279
<211> 56
<212> DNA
<213> Artificial Sequence

<220>
<223> oligo that mutates VH11 L to S

<400> 279
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<210> 280
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> 3' oligo for amplifying IgG1 constant regions

<400> 280
gtctctagac tatcatttac ccggagacag 30

<210> 281
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> 5' oligo for first PCR to insert IgA hinge into
      IgG1 CH2-CH3

<400> 281
ccatctccct caactccacc taccccatct ccctcatgcy cacctgaact cctg 54

<210> 282
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> 5' oligo for second PCR to insert IgA hinge into
      fused to IgG1 CH2

<400> 282
gttggtgatc agccagttcc ctcaactcca cctaccccat ctccccaact 50

<210> 283
<211> 1536
<212> DNA
<213> Artificial Sequence

<220>
<223> fusion polynucleotide

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt

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ccaggggaga aggtcacat gacttgcagg gccagctcaa gtgtaagtta catgactgg 180
taccagcaga agccaggatc ctccccaaa ccctggattt atgccccatc caacctggct 240
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agcagagtgg aggtgaaga tgctgccact tattactgcc agcagtggag ttttaacca 360
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<210> 284
<211> 505
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion polypeptide

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20 25 30
Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser
35 40 45
Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser
50 55 60
Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro
65 70 75 80
Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
85 90 95
Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
100 105 110
Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
115 120 125
Asp Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Ser
130 135 140
Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala
145 150 155 160
Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
165 170 175
Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile
180 185 190
Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
195 200 205
Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
210 215 220
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
225 230 235 240
Ala Arg Val Val Tyr Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp
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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt

Gly	Thr	Gly	Thr	Val	Thr	Val	Ser	Asp	Gln	Pro	Val	Pro	Ser	Thr
Pro	Pro	Thr	Pro	Ser	Pro	Ser	Thr	Pro	Pro	Thr	Pro	Ser	Pro	Cys
Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Lys
Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys
Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Tyr
Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu
Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	His
Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Lys
Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gln
Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Leu
Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Pro
Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn
Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Leu
Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Val
Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Gln
Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys						

<210> 285
<211> 1584
<212> DNA
<213> Artificial Sequence

<220>
<223> fusion polynucleotide

<400> 285

aagcttgccg	ccatggattt	tcaagtgcag	attttcagct	tcctgcta	cagtgcctca	60
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ccaggggaga	aggtcacaat	gacttgacag	gccagctcaa	gtgtaagta	catgcactgg	180
taccagcaga	agccaggatc	ctccccaaa	ccctggattt	atgccccatc	caacctggct	240
tctggagtc	ctgctcgctt	cagtggcagt	gggtctggga	cctcttactc	tctcacaatc	300
agcagagtgg	aggctgaaga	tgctgccact	tattactgcc	agcagtggag	ttttaaccca	360
cccacgttcg	gtgctgggac	caagctggag	ctgaaaagatg	gcggtggctc	ggcggtggtg	420
ggatctggag	gaggtgggag	ctctcaggct	tatctacagc	agtctggggc	tgagctgggtg	480
aggcctgggg	cctcagtga	gatgtcctgc	aaggctctcg	gctacacatt	taccagttac	540
aatatgcact	gggtaaagca	gacacctaga	cagggcctgg	aatggattgg	agctatttat	600
ccaggaaatg	gtgatacttc	ctacaatcag	aagttcaagg	gcaaggccac	actgactgta	660
gacaaatcct	ccagcacagc	ctacatgcag	ctcagcagcc	tgacatctga	agactctcg	720
gtctatttct	gtgcaagagt	gggtacttat	agtaactctt	actgtacttt	cgatgtctgg	780
ggcacagggg	ccacggtcac	cgctctctct	gatcagccag	ttccctcaac	tccacctacc	840
ccatctccct	caactccacc	tacctcatct	ccctcatgct	gccacccccg	actgtcactg	900
caccgaccgg	ccctcgagga	cctgctctta	gggttcagaa	cgatcctcac	gtgcacactg	960
accggcctga	gagatgcctc	agggtgcacc	ttcacctgga	cgccctcaag	tggaagagac	1020
gctgttcaag	gaccacctga	ccgtgacctc	tgtggctgct	acagcgtgtc	cagtgtcctg	1080
ccgggctgtg	ccgagccatg	gaaccatggg	aagacccttc	cttgacttgc	tgccctaccc	1140
gagtcacaaga	ccccgctaac	cgccaccctc	tcaaaatccg	gaaacacatt	ccggccccgag	1200
gtccacctgc	tgccgcccgc	gtcggaggag	ctggccctga	acgagctggt	gacgtgacg	1260
tgccctggcac	gtggcttcag	cccccaaggat	gtgctgggtc	gctggctgca	ggggtcacag	1320
gagctgcccc	gcgagaagta	cctgacttgg	gcattccccg	aggagccag	ccagggcacc	1380
accaccttcg	ctgtgaccag	catactgcgc	gtggcagccg	aggactggaa	gaagggggac	1440
accttctcct	gcatgggtgg	ccacgaggcc	ctgccgctgg	ccttcacaca	gaagaccatc	1500

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
gaccgcttgg cgggtaaacc cacccatgtc aatgtgtctg ttgtcatggc ggaggtggac 1560
ggcacctgct actgataatc taga 1584

<210> 286
<211> 520
<212> PRT
<213> Artificial sequence

<220>
<223> fusion polypeptide

<400> 286
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
1 5 10 15
Val Ile Ile Ala Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile
20 25 30
Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser
35 40 45
Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser
50 55 60
Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro
65 70 75 80
Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
85 90 95
Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
100 105 110
Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Leu Lys
115 120 125
Asp Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Ser
130 135 140
Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala
145 150 155 160
Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
165 170 175
Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile
180 185 190
Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
195 200 205
Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Thr Ala Tyr
210 215 220
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
225 230 235 240
Ala Arg Val Val Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp
245 250 255
Gly Thr Gly Thr Thr Val Thr Val Ser Ser Asp Gln Pro Val Pro Ser
260 265 270
Thr Pro Pro Thr Pro Ser Pro Ser Thr Pro Pro Thr Pro Ser Ser
275 280 285
Cys Cys His Pro Arg Leu Ser Leu His Arg Pro Ala Leu Glu Asp Leu
290 295 300
Leu Leu Gly Ser Glu Ala Ile Leu Thr Cys Thr Leu Thr Gly Leu Arg
305 310 315 320
Asp Ala Ser Gly Val Thr Phe Thr Trp Thr Pro Ser Ser Gly Lys Ser
325 330 335
Ala Val Gln Gly Pro Pro Asp Arg Asp Leu Cys Gly Cys Tyr Ser Val
340 345 350
Ser Ser Val Leu Pro Gly Cys Ala Glu Pro Trp Asn His Gly Lys Thr
355 360 365
Phe Thr Cys Thr Ala Ala Tyr Pro Glu Ser Lys Thr Pro Leu Thr Ala
370 375 380
Thr Leu Ser Lys Ser Gly Asn Thr Phe Arg Pro Glu Val His Leu Leu
385 390 395 400
Pro Pro Pro Ser Glu Leu Ala Leu Asn Glu Leu Val Thr Leu Thr
405 410 415
Cys Leu Ala Arg Gly Phe Ser Pro Lys Asp Val Leu Val Arg Trp Leu
420 425 430
Gln Gly Ser Gln Glu Leu Pro Arg Glu Lys Tyr Leu Thr Trp Ala Ser
435 440 445
Arg Gln Glu Pro Ser Gln Gly Thr Thr Thr Phe Ala Val Thr Ser Ile

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49076.000004pct2_10.207.655 Seq List Text 07.24.03.txt
 450 455 460
 Leu Arg Val Ala Ala Glu Asp Trp Lys Lys Gly Asp Thr Phe Ser Cys
 465 470 475 480
 Met Val Gly His Glu Ala Leu Pro Leu Ala Phe Thr Gln Lys Thr Ile
 485 490 495
 Asp Arg Leu Ala Gly Lys Pro Thr His Val Asn Val Ser Val Met
 500 505 510
 Ala Glu Val Asp Gly Thr Cys Tyr
 515 520

<210> 287
 <211> 775
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> fusion polynucleotide

<400> 287
 tgatcagcca gttccctcaa ctccacctac cccatctccc tcaactccac ctaccccatc 60
 tccctcatgc tgcaccccc gactgtcact gcaccgaccg gccctcgagg acctgtcttt 120
 aggttcagaa gcgacacctc cgtgcacact gaccggcctg agagatgcct caggtgtcac 180
 ctccacctgg acgcccctca gtgggaagag cgctgttcaa ggaccacctg accgtgacct 240
 ctgtggctgc tacagcgtgt ccagtgtcct gccgggctgt gccgagccat ggaaccatgg 300
 gaagaccttc acttgacctg ctgcctaccc cgagtccaag accccgctaa ccgccaccct 360
 ctcaaaatcc ggaaacacat tccggcccga ggtccacctg ctgccgccgc cgtcggagga 420
 gctggccctg aacgagctgg tgacgctgac gtgcctggca cgtggcttca gcccgaagga 480
 tgtgctggtt cgctggctgc aggggtcaca ggagctgccc cgcgagaagt acctgacttg 540
 ggcatcccgg caggagccca gccagggcac caccaccttc gctgtgacca gcatactgcg 600
 cgtggcagcc gaggactgga agaaggggga cacccttctc tgcattggtg gccacgaggg 660
 cctgccgctg gccttcacac agaagaccat cgaccgcttg gcgggtaaac ccaccatgt 720
 caatgtgtct gttgtcatgg cggaggtgga cggcacctgc tactgataat ctaga 775

<210> 288
 <211> 254
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> fusion polypeptide

<400> 288
 Asp Gln Pro Val Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Thr Pro
 1 5 10 15
 Pro Thr Pro Ser Pro Ser Cys Cys His Pro Arg Leu Ser Leu His Arg
 20 25 30
 Pro Ala Leu Glu Asp Leu Leu Leu Gly Ser Glu Ala Ile Leu Thr Cys
 35 40 45
 Thr Leu Thr Gly Leu Arg Asp Ala Ser Gly Val Thr Phe Thr Trp Thr
 50 55 60
 Pro Ser Ser Gly Lys Ser Ala Val Gln Gly Pro Pro Asp Arg Asp Leu
 65 70 75 80
 Cys Gly Cys Tyr Ser Val Ser Ser Val Leu Pro Gly Cys Ala Glu Pro
 85 90 95
 Trp Asn His Gly Lys Thr Phe Thr Cys Thr Ala Ala Tyr Pro Glu Ser
 100 105 110
 Lys Thr Pro Leu Thr Ala Thr Leu Ser Lys Ser Gly Asn Thr Phe Arg
 115 120 125
 Pro Glu Val His Leu Leu Pro Pro Pro Ser Glu Glu Leu Ala Leu Asn
 130 135 140
 Glu Leu Val Thr Leu Thr Cys Leu Ala Arg Gly Phe Ser Pro Lys Asp
 145 150 155 160
 Val Leu Val Arg Trp Leu Gln Gly Ser Gln Glu Leu Pro Arg Glu Lys
 165 170 175
 Tyr Leu Thr Trp Ala Ser Arg Gln Glu Pro Ser Gln Gly Thr Thr Thr
 180 185 190
 Phe Ala Val Thr Ser Ile Leu Arg Val Ala Ala Glu Asp Trp Lys Lys
 195 200 205

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
Gly Asp Thr Phe Ser Cys Met Val Gly His Glu Ala Leu Pro Leu Ala
210 215 220
Phe Thr Gln Lys Thr Ile Asp Arg Leu Ala Gly Lys Pro Thr His Val
225 230 235 240
Asn Val Ser Val Val Met Ala Glu Val Asp Gly Thr Cys Tyr
245 250

<210> 289
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> 3' oligo to PCR IgA hinge-CH2 CH3

<400> 289
gttgtttcta gattatcagt agcagggtgcc gtccacctcc gccatgacaa c 51

<210> 290
<211> 429
<212> DNA
<213> Artificial Sequence

<220>
<223> fusion polynucleotide

<400> 290
agatctcaag aagatgaaag gattgttctt gttgacaaca aatgtaagtg tgcccggtatt 60
acttccagga tcatccgttc ttccgaagat cctaattgagg acattgtgga gagaaacatc 120
cgaattattg ttctcttgaa caacagggag aatatctctg atcccacctc accattgaga 180
accagatttg tgtaccattt gtctgacctc agctgtaaaa aatgtgatcc tacagaagtg 240
gagctggata atcagatagt tactgctacc cagagcaata tctgtgatga agacagtgtc 300
acagagacct gctacactta tgacagaaac aagtgtctaca cagctgtggt cccactcgta 360
tatggtggtg agacaaaat ggtggaaaca gccttaacctc cagatgcctg ctatcctgac 420
taatctaga 429

<210> 291
<211> 139
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion polypeptide

<400> 291
Arg Ser Gln Glu Asp Glu Arg Ile Val Leu Val Asp Asn Lys Cys Lys
1 5 10 15
Cys Ala Arg Ile Thr Ser Arg Ile Ile Arg Ser Ser Glu Asp Pro Asn
20 25 30
Glu Asp Ile Val Glu Arg Asn Ile Arg Ile Ile Val Pro Leu Asn Asn
35 40 45
Arg Glu Asn Ile Ser Asp Pro Thr Ser Pro Leu Arg Thr Arg Phe Val
50 55 60
Tyr His Leu Ser Asp Leu Ser Cys Lys Lys Cys Asp Pro Thr Glu Val
65 70 75 80
Glu Leu Asp Asn Gln Ile Val Thr Ala Thr Gln Ser Asn Ile Cys Asp
85 90 95
Glu Asp Ser Ala Thr Glu Thr Cys Tyr Thr Tyr Asp Arg Asn Lys Cys
100 105 110
Tyr Thr Ala Val Val Pro Leu Val Tyr Gly Gly Glu Thr Lys Met Val
115 120 125
Glu Thr Ala Leu Thr Pro Asp Ala Cys Tyr Pro
130 135

<210> 292
<211> 36
<212> DNA

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
<213> Artificial Sequence

<220>

<223> 5' oligo to PCR J chain

<400> 292

gttgtagat ctcaagaaga tgaaaggatt gttctt 36

<210> 293

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> 3' oligo to PCR J chain

<400> 293

gttgtttcta gattagtcag gatagcaggc atctgg 36

<210> 294

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> 4 carboxy terminal amino acids deleted from IgA
CH3

<400> 294

Gly Thr Cys Tyr
1

<210> 295

<211> 763

<212> DNA

<213> Artificial Sequence

<220>

<223> fusion polynucleotide

<400> 295

tgatcagcca	gttccctcaa	ctccacctac	cccatctccc	tcaactccac	ctaccccatc	60
tccctcatgc	tgccaccccc	gactgtcact	gcaccgaccg	gccctcgagg	acctgctctt	120
aggttcagaa	gcgatcctca	cgtgcacact	gaccggcctg	agagatgcct	caggtgtcac	180
cttcacctgg	acgccctcaa	gtgggaagag	cgctgttcaa	ggaccacctg	accgtgacct	240
ctgtggctgc	tacagcgtgt	ccagtgtcct	gccgggctgt	gccgagccat	ggaaccatgg	300
gaagaccttc	acttgactg	ctgcctaccc	cgagtccaag	accccgctaa	ccgccaccct	360
ctcaaaatcc	ggaaacacat	tccggcccga	ggtccacctg	ctgccgccgc	cgtcggagga	420
gctggccctg	aacgagctgg	tgacgctgac	gtgcctggca	cgtaggcttca	gccccaaagga	480
tgtgctggtt	cgctggctgc	aggggtcaca	ggagctgccc	cgcgagaagt	acctgacttg	540
ggcatcccgg	caggagccca	gccagggcac	caccaccttc	gctgtgacca	gcatactgcg	600
cgtggcagcc	gaggactgga	agaaggggga	caccttctcc	tgcatgggtg	gccacgaggc	660
cctgccgctg	gccttcacac	agaagaccat	cgaccgcttg	gcgggtaaac	ccaccatgt	720
caatgtgtct	gttgtcatgg	cggaggtgga	ctgataatct	aga		763

<210> 296

<211> 250

<212> PRT

<213> Artificial Sequence

<220>

<223> fusion polypeptide

<400> 296

Asp	Gln	Pro	Val	Pro	Ser	Thr	Pro	Pro	Thr	Pro	Ser	Pro	Ser	Thr	Pro
1									10					15	
Pro	Thr	Pro	Ser	Pro	Ser	Cys	Cys	His	Pro	Arg	Leu	Ser	Leu	His	Arg
								25						30	

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PCT/US2003/024918

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
Pro Ala Leu Glu Asp Leu Leu Leu Gly Ser Glu Ala Ile Leu Thr Cys
35 40 45
Thr Leu Thr Gly Leu Arg Asp Ala Ser Gly Val Thr Phe Thr Trp Thr
50 55 60
Pro Ser Ser Gly Lys Ser Ala Val Gln Gly Pro Pro Asp Arg Asp Leu
65 70 75 80
Cys Gly Cys Tyr Ser Val Ser Ser Val Leu Pro Gly Cys Ala Glu Pro
85 90 95
Trp Asn His Gly Lys Thr Phe Thr Cys Thr Ala Ala Tyr Pro Glu Ser
100 105 110
Lys Thr Pro Leu Thr Ala Thr Leu Ser Lys Ser Gly Asn Thr Phe Arg
115 120 125
Pro Glu Val His Leu Leu Pro Pro Pro Ser Glu Glu Leu Ala Leu Asn
130 135 140
Glu Leu Val Thr Leu Thr Cys Leu Ala Arg Gly Phe Ser Pro Lys Asp
145 150 155 160
Val Leu Val Arg Trp Leu Gln Gly Ser Gln Glu Leu Pro Arg Glu Lys
165 170 175
Tyr Leu Thr Trp Ala Ser Arg Gln Glu Pro Ser Gln Gly Thr Thr Thr
180 185 190
Phe Ala Val Thr Ser Ile Leu Arg Val Ala Ala Glu Asp Trp Lys Lys
195 200 205
Gly Asp Thr Phe Ser Cys Met Val Gly His Glu Ala Leu Pro Leu Ala
210 215 220
Phe Thr Gln Lys Thr Ile Asp Arg Leu Ala Gly Lys Pro Thr His Val
225 230 235 240
Asn Val Ser Val Val Met Ala Glu Val Asp
245 250

<210> 297
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> 3' oligo for construct with 4 amino acid deletion
in IgA CH3

<400> 297
gttgtttcta gattatcagt ccacctccgc catgacaaca gacac

45

<210> 298
<211> 1572
<212> DNA
<213> Artificial Sequence

<220>
<223> fusion polynucleotide

<400> 298
aagcttgccg ccatggattt tcaagtgcag attttcagct tcctgctaatt cagtgtcttca 60
gtcataattg ccagaggaca aattgttctc tcccagcttc cagcaatcct gtctgcatct 120
ccaggggaga aggtcacaat gacttgcagg gccagctcaa gtgtaagtta catgcactgg 180
taccagcaga agccaggatc ctccccaaa ccctggattt atgccccatc caacctggct 240
tctggagtcc ctgctcgctt cagtggcagt gggctctggga cctcttactc tctcacaatc 300
agcagagtgg aggtgaaga tgctgccact tattactgcc agcagtggag tttaacca 360
cccacgttcg gtgctgggac caagctggag ctgaaagatg gcggtggctc gggcggtggg 420
ggatctggag gaggtgggag ctctcaggct tatctacagc agtctggggc tgagctgggt 480
aggcctgggg cctcagtga gatgtctgc aaggcttctg gctacacatt taccagttac 540
aatatgcact gggtaaaagca gacacctaga cagggcctgg aatggattgg agctatttat 600
ccaggaaatg gtgatacttc ctacaatcag aagttcaagg gcaaggccac actgactgta 660
gacaaatcct ccagcacagc ctacatgcag ctacagagc tgacatctga agactctgcg 720
gtctatttct gtgcaagagt ggtgtactat agtaactctt actgggtactt cgatgtctgg 780
ggcacaggga ccacggtcac cgtctcttct gatcagccag ttccctcaac tccacctacc 840
ccatctccct caactccacc taccctatct ccctatgct gccacccccg actgtcactg 900
caccgaccgg ccctcgagga cctgtcttta gttcagaag cgatcctcac tgggaagagc 960
accggtctga gagatgcctc aggtgtcacc ttacactgga cgccctcaag tgggaagagc 1020
gctgttcaag gaccactga ccgtgacctc tgtggctgct acagcgtgtc cagtgtcctg 1080

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 ccgggctgtg ccgagccatg gaaccatggg aagacattca cttgactgac tgcctacccc 1140
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 gtccacctgc tgccgccgcc gtcggaggag ctggccctga acgagctggt gacgctgacg 1260
 tgcttggcac gtggcttcag cccaaggat gtgctgggtc gctggctgca ggggtcacag 1320
 gagctgcccc gcgagaagta cctgacttgg gcatcccggc aggagcccag ccagggcacc 1380
 accaccttcg ctgtgaccag catactgctc gtggcagccg aggactggaa gaagggggac 1440
 accttctcct gcatgggtgg ccacgagggc ctgccgctgg ccttcacaca gaagaccatc 1500
 gaccgcttgg cgggtaaac caccatgtc aatgtgtctg ttgtcatggc ggaggtggac 1560
 tgataatcta ga 1572

<210> 299
 <211> 516
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> fusion polypeptide

<400> 299
 Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1 5 10 15
 Val Ile Ile Ala Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile
 20 25 30
 Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser
 35 40 45
 Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser
 50 55 60
 Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro
 65 70 75 80
 Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
 85 90 95
 Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
 100 105 110
 Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
 115 120 125
 Asp Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Ser
 130 135 140
 Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala
 145 150 155 160
 Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
 165 170 175
 Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile
 180 185 190
 Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
 195 200 205
 Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
 210 215 220
 Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
 225 230 235 240
 Ala Arg Val Val Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp
 245 250 255
 Gly Thr Gly Thr Thr Val Thr Val Ser Ser Asp Gln Pro Val Pro Ser
 260 265 270
 Thr Pro Pro Thr Pro Ser Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser
 275 280 285
 Cys Cys His Pro Arg Leu Ser Leu His Arg Pro Ala Leu Glu Asp Leu
 290 295 300
 Leu Leu Gly Ser Glu Ala Ile Leu Thr Cys Thr Leu Thr Gly Leu Arg
 305 310 315 320
 Asp Ala Ser Gly Val Thr Phe Thr Trp Thr Pro Ser Ser Gly Lys Ser
 325 330 335
 Ala Val Gln Gly Pro Pro Asp Arg Asp Leu Cys Gly Cys Tyr Ser Val
 340 345 350
 Ser Ser Val Leu Pro Gly Cys Ala Glu Pro Trp Asn His Gly Lys Thr
 355 360 365
 Phe Thr Cys Thr Ala Ala Tyr Pro Glu Ser Lys Thr Pro Leu Thr Ala
 370 375 380
 Thr Leu Ser Lys Ser Gly Asn Thr Phe Arg Pro Glu Val His Leu Leu
 385 390 395 400

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
Pro Pro Pro Ser Glu Glu Leu Ala Leu Asn Glu Leu Val Thr Leu Thr
405 410 415
Cys Leu Ala Arg Gly Phe Ser Pro Lys Asp Val Leu Val Arg Trp Leu
420 425 430
Gln Gly Ser Gln Glu Leu Pro Arg Glu Lys Tyr Leu Thr Trp Ala Ser
435 440 445
Arg Gln Glu Pro Ser Gln Gly Thr Thr Thr Phe Ala Val Thr Ser Ile
450 455 460
Leu Arg Val Ala Ala Glu Asp Trp Lys Lys Gly Asp Thr Phe Ser Cys
465 470 475 480
Met Val Gly His Glu Ala Leu Pro Leu Ala Phe Thr Gln Lys Thr Ile
485 490 495
Asp Arg Leu Ala Gly Lys Pro Thr His Val Asn Val Ser Val Val Met
500 505 510
Ala Glu Val Asp
515

<210> 300
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> 14 amino acids deleted from IgAH-T4 (so that total
of 18 amino acids deleted from wild type IgA CH3

<400> 300
Pro Thr His Val Asn Val Ser Val Val Met Ala Glu Val Asp
1 5 10

<210> 301
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> 3' oligo for engineering 14 amino acid from IgA-T4

<400> 301
gttggtttcta gattatcatt taccgcgcaa gcggtcgatg gtctt 45

<210> 302
<211> 709
<212> DNA
<213> Artificial Sequence

<220>
<223> fusion polynucleotide

<400> 302
tgatcagcca gttccctcaa ctccacctac cccatctccc tcaactccac ctaccccatc 60
tccctcatgc tgccaccccc gactgtcact gcaccgaccg gccctcgagg acctgtctctt 120
agggttcagaa gcgacccctca cgtgcacact gaccggcctg agagatgcct cagggtgtcac 180
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ctgtggctgc tacagcgtgt ccagtgtcct gccgggctgt gccgagccat ggaaccatgg 300
gaagaccttc acttgacttg ctgcctaccc cgagtccaag accccgctaa ccgccaccct 360
ctcaaaatcc ggaaacacat tccggcccga ggtccacctg ctgcccggcg cgtcggagga 420
gctggccctg aacgagctgg tgacgtgac gtgcctggca cgtggcttca gccccaagga 480
tgtgctggtt cgctggctgc aggggtcaca ggagctgccc cgcgagaagt acctgacttg 540
ggcatcccgg caggagccca gccagggcac caccaccttc gctgtgacca gcatactgcg 600
cgtggcagcc gaggactgga agaaggggga caccttctcc tgcattggtg gccacgaggc 660
cctgccgctg gccttcacac agaagaccat cgaccgcttg gcgggtaaa 709

<210> 303
<211> 236
<212> PRT
<213> Artificial Sequence

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<220>

<223> fusion polypeptide

<400> 303

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Pro Ala Leu Glu Asp Leu Leu Leu Gly Ser Glu Ala Ile Leu Thr Cys
 35     40     45
Thr Leu Thr Gly Leu Arg Asp Ala Ser Gly Val Thr Phe Thr Trp Thr
 50     55     60
Pro Ser Ser Gly Lys Ser Ala Val Gln Gly Pro Pro Asp Arg Asp Leu
 65     70     75
Cys Gly Cys Tyr Ser Val Ser Ser Val Leu Pro Gly Cys Ala Glu Pro
 85     90     95
Trp Asn His Gly Lys Thr Phe Thr Cys Thr Ala Ala Tyr Pro Glu Ser
100    105    110
Lys Thr Pro Leu Thr Ala Thr Leu Ser Lys Ser Gly Asn Thr Phe Arg
115    120    125
Pro Glu Val His Leu Leu Pro Pro Pro Ser Glu Glu Leu Ala Leu Asn
130    135    140
Glu Leu Val Thr Leu Thr Cys Leu Ala Arg Gly Phe Ser Pro Lys Asp
145    150    155
Val Leu Val Arg Trp Leu Gln Gly Ser Gln Glu Leu Pro Arg Glu Lys
160    165    170
Tyr Leu Thr Trp Ala Ser Arg Gln Glu Pro Ser Gln Gly Thr Thr Thr
180    185    190
Phe Ala Val Thr Ser Ile Leu Arg Val Ala Ala Glu Asp Trp Lys Lys
195    200    205
Gly Asp Thr Phe Ser Cys Met Val Gly His Glu Ala Leu Pro Leu Ala
210    215    220
Phe Thr Gln Lys Thr Ile Asp Arg Leu Ala Gly Lys
225    230    235

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<210> 304

<211> 1518

<212> DNA

<213> Artificial Sequence

<220>

<223> fusion polynucleotide

<400> 304

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gtcataattg ccagaggaca aattgtttct tcccagctct cagcaatcct gtctgcatct 120
ccaggggaga aggtcacaat gacttgcagg gccagctcaa gtgtaagtta catgcactgg 180
taccagcaga agccaggatc ctcccccaaa ccctggattt atgccccatc caacctggct 240
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cccacgttcg gtgctgggac caagctggag ctgaaagatg gcggtggctc gggcgggtgt 420
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aggcctgggg cctcagtga gatgtcctgc aaggcttctg gctacacatt taccagttac 540
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ccaggaaatg gtgatacttc ctacaatcag aagttcaagg gcaaggccac actgactgta 660
gacaaatcct ccagcacagc ctacatgcag ctacagagcc tgacatctga agactctgct 720
gtctatttct gtgcaagagt ggtgtactat agtaactctt actggtactt cgtgtctgtg 780
ggcagaggga ccacggtcac cgtctcttct gatcagccag tccctcaac tccacctacc 840
ccatctccct caactccacc taccctatct cctcatgct gccaccccg actgtcac tg 900
caccgaccgg ccctcgagga cctgctctta ggttcagaag cgatcctcac gtgcacactg 960
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ccgggctgtg ccgagccatg gaaccatggg aagaccttca cttgcaactg tgcctacc cc 1140
gagtccaaga ccccgctaac cgccacctc tcaaaatccg gaaacacatt ccggcccg ag 1200
gtccacctgc tgccgcccgc gtcggaggag ctggccctga acgagctggg gacgtgac cg 1260
tgccctggcac gtggcttcag cccaaggat gtgctgtgtc gctggctgca ggggtcac ag 1320
gagctgcccc gcgagaagta cctgacttgg gcatcccgcc aggagcccag ccagggca cc 1380

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accttctcct gcatgggtgg ccacgagggc ctgccgctgg ccttcacaca gaagaccatc 1500
gaccgcttgg cgggtaaa 1518

<210> 305
<211> 502
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion polypeptide

<400> 305
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
1 5 10 15
Val Ile Ile Ala Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile
20 25 30
Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser
35 40 45
Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser
50 55 60
Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro
65 70 75 80
Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
85 90 95
Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
100 105 110
Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
115 120 125
Asp Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Ser
130 135 140
Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala
145 150 155 160
Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
165 170 175
Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile
180 185 190
Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
195 200 205
Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
210 215 220
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
225 230 235 240
Ala Arg Val Val Tyr Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp
245 250 255
Gly Thr Gly Thr Thr Val Thr Val Ser Ser Asp Gln Pro Val Pro Ser
260 265 270
Thr Pro Pro Thr Pro Ser Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser
275 280 285
Cys Cys His Pro Arg Leu Ser Leu His Arg Pro Ala Leu Glu Asp Leu
290 295 300
Leu Leu Gly Ser Glu Ala Ile Leu Thr Cys Thr Leu Thr Gly Leu Arg
305 310 315 320
Asp Ala Ser Gly Val Thr Phe Thr Trp Thr Pro Ser Ser Gly Lys Ser
325 330 335
Ala Val Gln Gly Pro Pro Asp Arg Asp Leu Cys Gly Cys Tyr Ser Val
340 345 350
Ser Ser Val Leu Pro Gly Cys Ala Glu Pro Trp Asn His Gly Lys Thr
355 360 365
Phe Thr Cys Thr Ala Ala Tyr Pro Glu Ser Lys Thr Pro Leu Thr Ala
370 375 380
Thr Leu Ser Lys Ser Gly Asn Thr Phe Arg Pro Glu Val His Leu Leu
385 390 395 400
Pro Pro Pro Ser Glu Glu Leu Ala Leu Asn Glu Leu Val Thr Leu Thr
405 410 415
Cys Leu Ala Arg Gly Phe Ser Pro Lys Asp Val Leu Val Arg Trp Leu
420 425 430
Gln Gly Ser Gln Glu Leu Pro Arg Glu Lys Tyr Leu Thr Trp Ala Ser
435 440 445

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
 Arg Gln Glu Pro Ser Gln Gly Thr Thr Thr Phe Ala Val Thr Ser Ile
 450 455 460
 Leu Arg Val Ala Ala Glu Asp Trp Lys Lys Gly Asp Thr Phe Ser Cys
 465 470 475 480
 Met Val Gly His Glu Ala Leu Pro Leu Ala Phe Thr Gln Lys Thr Ile
 485 490 495
 Asp Arg Leu Ala Gly Lys
 500

<210> 306
 <211> 924
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> fusion polynucleotide

<400> 306
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 tacatctgca aggtggagct catgtaccca ccgccatact acctgggcat aggcaacgga 180
 acccagattt atgtaattga tccagaaccg tgcccagatt ctgatcaacc caaatcttgt 240
 gacaaaactc acacatgccc accgtgccc gcacctgaac tcctgggggg accgtcagtc 300
 ttctcttcc cccaaaacc caaggacacc ctcatgatct cccggacccc tgaggtcaca 360
 tgcgtggtgg tggacgtgag ccacgaagac cctgaggtca agttcaactg gtacgtggac 420
 ggctgtggagg tgcataatgc caagacaaag ccgctggagg agcagtacaa cagcacgtac 480
 cgtgtggtca gcgtctctac cgtctgcac caggactggc tgaatggcaa ggagtacaag 540
 tgcaagggtc ccaacaaagc cctcccagcc cccatcgaga aaacaatctc caaagccaaa 600
 gggcagcccc gagaaccaca ggtgtacacc ctgcccccat cccgggatga gctgaccaag 660
 aaccaggtca gcctgacctg cctggtcaaa ggcttctatc ccagcgacat cgccgtggag 720
 tgggagagca atgggcagcc ggagaacaac tacaagacca cgctcccgt gctggactcc 780
 gacggctcct tcttctctca cagcaagctc accgtggaca agagcagggtg gcagcagggg 840
 aacgtcttct catgctccgt gatgcatgag gctctgcaca accactacac gcagaagagc 900
 ctctccctgt ctccgggtaa atga 924

<210> 307
 <211> 382
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> fusion polypeptide

<400> 307
 Met Gly Val Leu Leu Thr Gln Arg Thr Leu Leu Ser Leu Val Leu Ala
 1 5 10 15
 Leu Leu Phe Pro Ser Met Ala Ser Met Ala Met His Val Ala Gln Pro
 20 25 30
 Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala Ser Phe Val Cys Glu
 35 40 45
 Tyr Ala Ser Pro Gly Lys Ala Thr Glu Val Arg Val Thr Val Leu Arg
 50 55 60
 Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala Ala Thr Tyr Met Met
 65 70 75 80
 Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser Ile Cys Thr Gly Thr Ser
 85 90 95
 Ser Gly Asn Gln Val Asn Leu Thr Ile Gln Gly Leu Arg Ala Met Asp
 100 105 110
 Thr Gly Leu Tyr Ile Cys Lys Val Glu Leu Met Tyr Pro Pro Tyr
 115 120 125
 Tyr Leu Gly Ile Gly Asn Gly Thr Gln Ile Tyr Val Ile Asp Pro Glu
 130 135 140
 Pro Cys Pro Asp Ser Asp Gln Pro Lys Ser Cys Asp Lys Thr His Thr
 145 150 155 160
 Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe
 165 170 175
 Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
 180 185 190

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
 Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
 195 200 205
 Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
 210 215 220
 Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
 225 230 235 240
 Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
 245 250 255
 Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
 260 265 270
 Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
 275 280 285
 Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
 290 295 300
 Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
 305 310 315 320
 Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
 325 330 335
 Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
 340 345 350
 Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
 355 360 365
 Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 370 375 380

<210> 308
 <211> 453
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> fusion polynucleotide

<400> 308
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 ggcatcgcca gctttgtgtg tgagtatgca tctccaggca aagccactga ggtccgggtg 180
 acagtgtctc ggcaggctga cagccagggtg actgaagtct gtgcggcaac ctacatgatg 240
 gggaatgagt tgaccttctt agatgattcc atctgcacgg gcacctccag tggaaatcaa 300
 gtgaacctca ctatccaagg actgagggcc atggacacgg gactctacat ctgcaagggtg 360
 gagctcatgt acccaccgcc atactacctg ggcataggca acggaacca gatttatgta 420
 attgatccag aaccgtgccc agattctgat caa 453

<210> 309
 <211> 151
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> fusion polypeptide

<400> 309
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 Leu Leu Phe Pro Ser Met Ala Ser Met Ala Met His Val Ala Gln Pro
 20 25 30
 Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala Ser Phe Val Cys Glu
 35 40 45
 Tyr Ala Ser Pro Gly Lys Ala Thr Glu Val Arg Val Thr Val Leu Arg
 50 55 60
 Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala Ala Thr Tyr Met Met
 65 70 75 80
 Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser Ile Cys Thr Gly Thr Ser
 85 90 95
 Ser Gly Asn Gln Val Asn Leu Thr Ile Gln Gly Leu Arg Ala Met Asp
 100 105 110
 Thr Gly Leu Tyr Ile Cys Lys Val Glu Leu Met Tyr Pro Pro Pro Tyr
 115 120 125

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
Tyr Leu Gly Ile Gly Asn Gly Thr Gln Ile Tyr Val Ile Asp Pro Glu
130 135 140
Pro Cys Pro Asp Ser Asp Gln
145 150

<210> 310
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> 5' oligo for engineering 14 amino acids from
IgA-T4

<400> 310
gttgtgatc agccagttcc ctcaactcca cctaccccat ctccctcaac t 51

<210> 311
<211> 75
<212> DNA
<213> Artificial Sequence

<220>
<223> fusion polynucleotide

<400> 311
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agcatggcga gcatg 75

<210> 312
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion polypeptide

<400> 312
Met Gly Val Leu Leu Thr Gln Arg Thr Leu Leu Ser Leu Val Leu Ala
1 5 10 15
Leu Leu Phe Pro Ser Met
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<210> 313
<211> 372
<212> DNA
<213> Artificial Sequence

<220>
<223> fusion polynucleotide

<400> 313
gcaatgcacg tggcccagcc tgctgtggta ctggccagca gccgagggcat cgccagcttt 60
gtgtgtgagt atgcatctcc aggc aaagcc actgaggtcc gggtagacagt gcttcggcag 120
gctgacagcc aggtgactga agtctgtgcg gcaacctaca tgacggggaa tgagttgacc 180
ttcctagatg attccatctg cacgggcacc tccagtggaa atcaagtga cctcactatc 240
caaggactga gggccatgga cacgggactc tacatctgca aggtggagct catgtacca 300
ccgccatact acctgggcat aggc aaaggga accagattt atgtaattga tccagaaccg 360
tgcccagatt ct 372

<210> 314
<211> 124
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion polypeptide

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Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly Lys Ala Thr Glu
 20      25      30
Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val
 35      40      45
Cys Ala Ala Thr Tyr Met Thr Gly Asn Glu Leu Thr Phe Leu Asp Asp
 50      55      60
Ser Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn Leu Thr Ile
 65      70      75      80
Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu
 85      90      95
Leu Met Tyr Pro Pro Pro Tyr Tyr Leu Gly Ile Gly Asn Gly Thr Gln
100      105      110
Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser
115      120
```

```
<210> 315
<211> 1149
<212> DNA
<213> Artificial Sequence
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<220>
<223> fusion polynucleotide
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<400> 315
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ggcatcgcca gctttgtgtg tgagtatgca tctccaggca aagccactga ggtccgggtg 180
acagtgcctc ggcaggctga cagccaggctg actgaagtct gtgcggcaac ctacatgatg 240
gggaatgagt tgaccttcct agatgattcc atctgcacgg gcacctccag tggaaatcaa 300
tggaacctca ctatccaagg actgagggcc atggacacgg gactctacat ctgcaagggtg 360
gagctcatgt acccaccgcc atactacctg ggcataggca acggaacca gatttatgta 420
attgatccag aaccgtgccc agattctgat caaccctaat cttctgacaa aactcacaca 480
tccccaccgt ccccgaccac tgaactcctg gggggatcgt cagtcttctt cttcccccca 540
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aatgccaaga caaagccgct ggaggagcag tacaacagca cgtaccgtgt ggtcagcgtc 720
ctcaccgtcc tgcaccagga ctggctgaat ggcaaggagt acaagtgcga ggtctccaac 780
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tccgtgatgc atgaggctct gcacaaccac tacacgcaga agagcctctc cctgtctccg 1140
ggtaaatga                                     1149
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<210> 316
<211> 382
<212> PRT
<213> Artificial Sequence
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```
<220>
<223> fusion polypeptide
```

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<400> 316
Met Gly Val Leu Leu Thr Gln Arg Thr Leu Leu Ser Leu Val Leu Ala
 1      5      10      15
Leu Leu Phe Pro Ser Met Ala Ser Met Ala Met His Val Ala Gln Pro
 20      25      30
Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala Ser Phe Val Cys Glu
 35      40      45
Tyr Ala Ser Pro Gly Lys Ala Thr Glu Val Arg Val Thr Val Leu Arg
 50      55      60
Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala Ala Thr Tyr Met Met
 65      70      75      80
```

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<400>	317						
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ggcatcgcca	gctttgtgtg	tgagtatgca	tctccaggca	aagccactga	ggtccgggtg	180	
acagtgcttc	ggcaggctga	cagccagggt	actgaagctc	gtgcggcaac	ctacatgatg	240	
gggaatgagt	tgaccttctc	agatgattcc	atctgcacgg	gcacctccag	tggaaatcaa	300	
gtgaacctga	ctatccaagg	actgagggcc	atggacacga	gactctacat	ctgcaaggtg	360	
gagctctatg	acccacgcgc	atactacctg	ggcataggca	acggaaccca	gatttatgta	420	
attgatccag	aaccgtgcc	agattctgat	cagccagttc	ccccaactcc	acctacccca	480	
tctccctcaa	ctccacctac	cccatctccc	tcagtctgcc	acccccgact	gtcactgcac	540	
cgacgggccc	tcgaggacct	gctcttaggt	tcagaagcga	tcctcacgtg	cacactgacc	600	
ggcctgagag	atgctctcag	tgctcacctc	acctggacgc	cctcaagtgg	gaagagcgct	660	
gttcaaggac	cacctgaccg	tgacctctgt	ggctgctaca	gcgtgtccag	tgctctgcg	720	
ggctgtgccc	agccatggaa	ccatgggaag	accttcactt	gcactgctgc	ctaccccgag	780	
tccaagacc	cgctaaccgc	cacctctcca	aaatccggaa	acacattccg	gcccgaggtc	840	
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ctggcacgtg	gcttcagccc	caaggatgtg	ctggttcgct	ggctgcagg	gtcacaggag	960	
ctgccccgcg	agaagtacat	gacttgggca	tccgggcagg	agcccagcca	gggcaccacc	1020	
accttcgctg	tgactagcat	actgcgcgtg	cgacgcgagg	actggaagaa	gggggacacc	1080	
ttctctctga	tgggtggcca	cgaggccctg	ccgctgcgct	tcacacagaa	gaccatcgac	1140	
cgcttggcgg	gtaaaccac	ccatgtcaat	gtgtctgttg	tcatggcgga	ggttgacgac	1200	

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
acctgtact gataatctag a

1221

<210> 318
<211> 403
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion polypeptide

<400> 318
Met Gly Val Leu Leu Thr Gln Arg Thr Leu Leu Ser Leu Val Leu Ala
1 5 10 15
Leu Leu Phe Pro Ser Met Ala Ser Met Ala Met His Val Ala Gln Pro
20 25 30
Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala Ser Phe Val Cys Glu
35 40 45
Tyr Ala Ser Pro Gly Lys Ala Thr Glu Val Arg Val Thr Val Leu Arg
50 55 60
Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala Ala Thr Tyr Met Met
65 70 75 80
Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser Ile Cys Thr Gly Thr Ser
85 90 95
Ser Gly Asn Gln Val Asn Leu Thr Ile Gln Gly Leu Arg Ala Met Asp
100 105 110
Thr Gly Leu Tyr Ile Cys Lys Val Glu Leu Met Tyr Pro Pro Tyr
115 120 125
Tyr Leu Gly Ile Gly Asn Gly Thr Gln Ile Tyr Val Ile Asp Pro Glu
130 135 140
Pro Cys Pro Asp Ser Asp Gln Pro Val Pro Ser Thr Pro Pro Thr Pro
145 150 155 160
Ser Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Cys Cys His Pro Arg
165 170 175
Leu Ser Leu His Arg Pro Ala Leu Glu Asp Leu Leu Leu Gly Ser Glu
180 185 190
Ala Ile Leu Thr Cys Thr Leu Thr Gly Leu Arg Asp Ala Ser Gly Val
195 200 205
Thr Phe Thr Trp Thr Pro Ser Ser Gly Lys Ser Ala Val Gln Gly Pro
210 215 220
Pro Asp Arg Asp Leu Cys Gly Cys Tyr Ser Val Ser Ser Val Leu Pro
225 230 235 240
Gly Cys Ala Glu Pro Trp Asn His Gly Lys Thr Phe Thr Cys Thr Ala
245 250 255
Ala Tyr Pro Glu Ser Lys Thr Pro Leu Thr Ala Thr Leu Ser Lys Ser
260 265 270
Gly Asn Thr Phe Arg Pro Glu Val His Leu Leu Pro Pro Ser Glu
275 280 285
Glu Leu Ala Leu Asn Glu Leu Val Thr Leu Thr Cys Leu Ala Arg Gly
290 295 300
Phe Ser Pro Lys Asp Val Leu Val Arg Trp Leu Gln Gly Ser Gln Glu
305 310 315 320
Leu Pro Arg Glu Lys Tyr Leu Thr Trp Ala Ser Arg Gln Glu Pro Ser
325 330 335
Gln Gly Thr Thr Thr Phe Ala Val Thr Ser Ile Leu Arg Val Ala Ala
340 345 350
Glu Asp Trp Lys Lys Gly Asp Thr Phe Ser Cys Met Val Gly His Glu
355 360 365
Ala Leu Pro Leu Ala Phe Thr Gln Lys Thr Ile Asp Arg Leu Ala Gly
370 375 380
Lys Pro Thr His Val Asn Val Ser Val Val Met Ala Glu Val Asp Gly
385 390 395 400
Thr Cys Tyr

<210> 319
<211> 1209
<212> DNA
<213> Artificial Sequence

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt

<220>

<223> fusion polynucleotide

<400> 319

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cgcttggcgg gtaaaccac ccatgtcaat gtgtctgttg tcatggcgga ggtggactga 1200
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<210> 320

<211> 399

<212> PRT

<213> Artificial Sequence

<220>

<223> fusion polypeptide

<400> 320

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Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala Ser Phe Val Cys Glu
35     40     45
Tyr Ala Ser Pro Gly Lys Ala Thr Glu Val Arg Val Thr Val Leu Arg
50     55     60
Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala Ala Thr Tyr Met Met
65     70     75     80
Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser Ile Cys Thr Gly Thr Ser
85     90     95
Ser Gly Asn Gln Val Asn Leu Thr Ile Gln Gly Leu Arg Ala Met Asp
100    105    110
Thr Gly Leu Tyr Ile Cys Lys Val Glu Leu Met Tyr Pro Pro Tyr
115    120    125
Tyr Leu Gly Ile Gly Asn Gly Thr Gln Ile Tyr Val Ile Asp Pro Glu
130    135    140
Pro Cys Pro Asp Ser Asp Gln Pro Val Pro Ser Thr Pro Pro Thr Pro
145    150    155    160
Ser Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Cys Cys His Pro Arg
165    170    175
Leu Ser Leu His Arg Pro Ala Leu Glu Asp Leu Leu Leu Gly Ser Glu
180    185    190
Ala Ile Leu Thr Cys Thr Leu Thr Gly Leu Arg Asp Ala Ser Gly Val
195    200    205
Thr Phe Thr Trp Thr Pro Ser Gly Lys Ser Ala Val Gln Gly Pro
210    215    220
Pro Asp Arg Asp Leu Cys Gly Cys Tyr Ser Val Ser Ser Val Leu Pro
225    230    235    240
Gly Cys Ala Glu Pro Trp Asn His Gly Lys Thr Phe Thr Cys Thr Ala
245    250    255
Ala Tyr Pro Glu Ser Lys Thr Pro Leu Thr Ala Thr Leu Ser Lys Ser

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
 260 265 270
 Gly Asn Thr Phe Arg Pro Glu Val His Leu Leu Pro Pro Pro Ser Glu
 275 280 285
 Glu Leu Ala Leu Asn Glu Leu Val Thr Leu Thr Cys Leu Ala Arg Gly
 290 295 300
 Phe Ser Pro Lys Asp Val Leu Val Arg Trp Leu Gln Gly Ser Gln Glu
 305 310 315 320
 Leu Pro Arg Glu Lys Tyr Leu Thr Trp Ala Ser Arg Gln Glu Pro Ser
 325 330 335
 Gln Gly Thr Thr Phe Ala Val Thr Ser Ile Leu Arg Val Ala Ala
 340 345 350
 Glu Asp Trp Lys Lys Gly Asp Thr Phe Ser Cys Met Val Gly His Glu
 355 360 365
 Ala Leu Pro Leu Ala Phe Thr Gln Lys Thr Ile Asp Arg Leu Ala Gly
 370 375 380
 Lys Pro Thr His Val Asn Val Ser Val Val Met Ala Glu Val Asp
 385 390 395

<210> 321
 <211> 328
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> fusion polynucleotide

<400> 321
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 gaggtcaagt tcaactggta cgtggacggc gtggaggtgc ataatgccaa gacaaagccg 180
 cgggaggagc agtacaacag cacgtaccgt gtggtcagcg tcctcaccgt cctgcaccag 240
 gactggctga atggcaagga gtacaagtgc aaggtctcca acaaagccct cccagccccc 300
 atcgagaaaa ccatctccaa agccaaag 328

<210> 322
 <211> 109
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> fusion polypeptide

<400> 322
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 1 5 10 15
 Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
 20 25 30
 Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
 35 40 45
 Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
 50 55 60
 Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
 65 70 75 80
 Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
 85 90 95
 Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
 100 105

<210> 323
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Amino acids surrounding the proline at 238

<400> 323

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PCT/US2003/024918

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser
1 5 10

<210> 324
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid substitution of Serine for Proline at
238

<400> 324
Pro Ala Pro Glu Leu Leu Gly Gly Ser Ser
1 5 10

<210> 325
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> 5' oligo to PCR IgE Fc

<400> 325
gttggtgac acgtctgctc cagggacttc acccc 35

<210> 326
<211> 49
<212> DNA
<213> Artificial Sequence

<220>
<223> 3' oligo to PCR IgE Fc

<400> 326
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<210> 327
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> oligo to provide open reading frame at carboxy end
of CH4 to read into transmembrane and cytoplasmic
tail of another protein

<400> 327
gttggttttcg aaggatccgc ttaccggga ttacagaca ccgctcgctg g 51

<210> 328
<211> 996
<212> DNA
<213> Artificial Sequence

<220>
<223> fusion polynucleotide

<400> 328
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ctttgaggac agcaccaaga agtgtgcaga ttccaacccg agaggggtga gcgcctacct 360
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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
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 gtccaccctg ccggtgggca cccgagactg gatcgagggg gagacctacc agtgcagggt 600
 gaccaccccc cacctgcccc gggccctcat gcggtccacg accaagacca gcggcccgcg 660
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 caccctcgcc tgcctgatcc agaacttcat gcctgaggac atctcgggtgc agtgggtgca 780
 caacgaggtg cagctcccgg acgcccggca cagcacgacg cagccccgca agaccaaggg 840
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<210> 329
 <211> 331
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> fusion polypeptide

<400> 329
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 20 25 30
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 35 40 45
 Leu Glu Asp Gly Gln Val Met Asp Val Asp Leu Ser Thr Ala Ser Thr
 50 55 60
 Thr Gln Glu Gly Glu Leu Ala Ser Thr Gln Ser Glu Leu Thr Leu Ser
 65 70 75 80
 Gln Lys His Trp Leu Ser Asp Arg Thr Tyr Thr Cys Gln Val Thr Tyr
 85 90 95
 Gln Gly His Thr Phe Glu Asp Ser Thr Lys Lys Cys Ala Asp Ser Asn
 100 105 110
 Pro Arg Gly Val Ser Ala Tyr Leu Ser Arg Pro Ser Pro Phe Asp Leu
 115 120 125
 Phe Ile Arg Lys Ser Pro Thr Ile Thr Cys Leu Val Val Asp Leu Ala
 130 135 140
 Pro Ser Lys Gly Thr Val Asn Leu Thr Trp Ser Arg Ala Ser Gly Lys
 145 150 155 160
 Pro Val Asn His Ser Thr Arg Lys Glu Glu Lys Gln Arg Asn Gly Thr
 165 170 175
 Leu Thr Val Thr Ser Thr Leu Pro Val Gly Thr Arg Asp Trp Ile Glu
 180 185 190
 Gly Glu Thr Tyr Gln Cys Arg Val Thr His Pro His Leu Pro Arg Ala
 195 200 205
 Leu Met Arg Ser Thr Thr Lys Thr Ser Gly Pro Arg Ala Ala Pro Glu
 210 215 220
 Val Tyr Ala Phe Ala Thr Pro Glu Trp Pro Gly Ser Arg Asp Lys Arg
 225 230 235 240
 Thr Leu Ala Cys Leu Ile Gln Asn Phe Met Pro Glu Asp Ile Ser Val
 245 250 255
 Gln Trp Leu His Asn Glu Val Gln Leu Pro Asp Ala Arg His Ser Thr
 260 265 270
 Thr Gln Pro Arg Lys Thr Lys Gly Ser Gly Phe Phe Val Phe Ser Arg
 275 280 285
 Leu Glu Val Thr Arg Ala Glu Trp Glu Gln Lys Asp Glu Phe Ile Cys
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 305 310 315 320
 Val Ser Val Asn Pro Gly Lys Ala Asp Pro Ser 330

<210> 330
 <211> 63
 <212> DNA
 <213> Artificial Sequence

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<220>

<223> fusion polynucleotide

<400> 330

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<210> 331

<211> 52

<212> DNA

<213> Artificial Sequence

<220>

<223> fusion polynucleotide

<400> 331

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<210> 332

<211> 91

<212> DNA

<213> Artificial Sequence

<220>

<223> fusion polynucleotide

<400> 332

gttgttgatc aggagcccaa atcttctgac aaaactcaca catctccacc gtccccagca 60
cctgaactcc tgggtggacc gtcagtcttc c 91

<210> 333

<211> 1800

<212> DNA

<213> Artificial Sequence

<220>

<223> fusion polynucleotide

<400> 333

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ccaggggaga aggtcacaat gacttgcagg gccagctcaa gtgtaagtta catgcactgg 180
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agccccctac agaccgtcca gcgagcgggtg tctgtaaatc ccgtaaatg ataactctaga 1800
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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt

<210> 334
<211> 592
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion polypeptide

<400> 334
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Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser
35 40 45
Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser
50 55 60
Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro
65 70 75 80
Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
85 90 95
Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
100 105 110
Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
115 120 125
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Ser
130 135 140
Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala
145 150 155 160
Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
165 170 175
Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile
180 185 190
Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
195 200 205
Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Thr Ala Tyr
210 215 220
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
225 230 235 240
Ala Arg Val Val Tyr Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp
245 250 255
Gly Thr Gly Thr Thr Val Thr Val Ser Asp His Val Cys Ser Arg Asp
260 265 270
Phe Thr Pro Thr Val Lys Ile Leu Gln Ser Ser Cys Asp Gly Gly
275 280 285
Gly His Phe Pro Pro Thr Ile Gln Leu Leu Cys Leu Val Ser Gly Tyr
290 295 300
Thr Pro Gly Thr Ile Asn Ile Thr Trp Leu Glu Asp Gly Gln Val Met
305 310 315 320
Asp Val Asp Leu Ser Thr Ala Ser Thr Thr Gln Glu Gly Glu Leu Ala
325 330 335
Ser Thr Gln Ser Glu Leu Thr Leu Ser Gln Lys His Trp Leu Ser Asp
340 345 350
Arg Thr Tyr Thr Cys Gln Val Thr Tyr Gln Gly His Thr Phe Glu Asp
355 360 365
Ser Thr Lys Lys Cys Ala Asp Ser Asn Pro Arg Gly Val Ser Ala Tyr
370 375 380
Leu Ser Arg Pro Ser Pro Phe Asp Leu Phe Ile Arg Lys Ser Pro Thr
385 390 395 400
Ile Thr Cys Leu Val Val Asp Leu Ala Pro Ser Lys Gly Thr Val Asn
405 410 415
Leu Thr Trp Ser Arg Ala Ser Gly Lys Pro Val Asn His Ser Thr Arg
420 425 430
Lys Glu Glu Lys Gln Arg Asn Gly Thr Leu Thr Val Thr Ser Thr Leu
435 440 445
Pro Val Gly Thr Arg Asp Trp Ile Glu Gly Glu Thr Tyr Gln Cys Arg

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt

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465	470	475													480				
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				485					490						495				
Glu	Trp	Pro	Gly	Ser	Arg	Asp	Lys	Arg	Thr	Leu	Ala	Cys	Leu	Ile	Gln				
			500					505						510					
Asn	Phe	Met	Pro	Glu	Asp	Ile	Ser	Val	Gln	Trp	Leu	His	Asn	Glu	Val				
		515					520					525							
Gln	Leu	Pro	Asp	Ala	Arg	His	Ser	Thr	Thr	Gln	Pro	Arg	Lys	Thr	Lys				
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Gly	Ser	Gly	Phe	Phe	Val	Phe	Ser	Arg	Leu	Glu	Val	Thr	Arg	Ala	Glu				
545					550				555						560				
Trp	Glu	Gln	Lys	Asp	Glu	Phe	Ile	Cys	Arg	Ala	Val	His	Glu	Ala	Ala				
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Ser	Pro	Ser	Gln	Thr	Val	Gln	Arg	Ala	Val	Ser	Val	Asn	Pro	Gly	Lys				
			580					585					590						

<210> 335
 <211> 339
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> fusion polynucleotide

<400> 335
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 ccaggaaagg gtctggaatg gatgggaata atatattatg atggaggcac agattataat 180
 tcagcaatta aatccagact gagcatcagc agggacacct ccaagagcca agttttctta 240
 aaaatcaaca gtctgcaaac tgatgacaca gccatgtatt actgtgccag aatccacttt 300
 gattactggg gccaaaggagt catggtcaca gtctcctct 339

<210> 336
 <211> 321
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> fusion polynucleotide

<400> 336
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 gcctccccta aactctggat ttatgacaca tccaagctgg cttctggagt tccaaatcgc 180
 ttccagtggca gtgggtctgg gacctcttat tctctcgcaa tcaacacccat ggagactgaa 240
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 accaagctgg agatcaaacg g 321

<210> 337
 <211> 785
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> fusion polynucleotide

<400> 337
 aagcttatgg attttcaagt gcagattttc agcttcctgc taatcagtgc ttcagtcata 60
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 cagcagaagt caggcgcttc ccctaaactc tggatttatg acacatcaa gctggcttct 240
 ggagtccaa atcgcttcag tggcagtggg tctgggacct cttattctct cgcaatcaac 300
 accatggaga ctgaagatgc tgccacttat tactgtcagc agtggagtag tactccgctc 360

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PCT/US2003/024918

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
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ccgacacaga ccctgtccct cacatgcact gtctctgggt tctcattaac cagcgaatggt 540
gtacactgga ttcgacagcc tccaggaaag ggtctggaat ggatgggaat aatatattat 600
gatggaggga cagattataa ttcagcaatt aaatccagac tgagcatcag cagggaacacc 660
tccaagagcc aagttttctt aaaaatcaac agtctgcaaa ctgatgacac agccatgtat 720
tactgtgcca gaatccactt tgattactgg ggccaaggag tcatggtcac agtctcctct 780
gatca 785

<210> 338
<211> 1491
<212> DNA
<213> Artificial Sequence

<220>
<223> fusion polynucleotide

<400> 338
aagcttatgg attttcaagt gcagattttc agcttcctgc taatcagtgc ttcagtcata 60
atgtccagag gagtgcacat tgtgtcact cagtctccaa caaccatagc tgcattctcca 120
ggggagaagg tcaccatcac ctgccgtgcc agctccagt taagttacat gtactgggtac 180
cagcagaagt caggcgctc ccctaaactc tggatttatg acacatccaa gctggcttct 240
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acgttcgggt ctgggaccaa gctggagatc aaacgggggtg gcggtggctc gggcgggtggt 420
gggtcgggtg gcggcggatc tcaggtgcag ctgaaggagg caggacctgg cctgggtgcaa 480
ccgacacaga ccctgtccct cacatgcact gtctctgggt tctcattaac cagcgaatggt 540
gtacactgga ttcgacagcc tccaggaaag ggtctggaat ggatgggaat aatatattat 600
gatggaggca cagattataa ttcagcaatt aaatccagac tgagcatcag cagggaacacc 660
tccaagagcc aagttttctt aaaaatcaac agtctgcaaa ctgatgacac agccatgtat 720
tactgtgcca gaatccactt tgattactgg ggccaaggag tcatggtcac agtctcctct 780
gatcaggagc ccaaactctg tgacaaaact cacacatgcc caccgtgcc agcacctgaa 840
ctcctggggg gaccgtcagt cttcctcttc cccccaaaac ccaaggacac cctcatgac 900
tcccggagcc ctgaggtcac atgcgtggtg gtggacctga gccacgaaga cctgaggtc 960
aagttcaact ggtacgtgga cggcgtggag gtgcataatg ccaagacaaa gccgcgggag 1020
gagcagtaca acagcacgta ccgtgtggtc agcgtcctca ccgtcctgca ccaggactgg 1080
ctgaatggca aggagtacaa gtgcaagggtc tccaacaaag ccctccagc ccccatcgag 1140
aaaacaatct ccaaagccaa agggcagccc cgagaaccac aggtgtacac cctgccccca 1200
tcccgggatg agctgaccaa gaaccagggtc agcctgacct gcctggtcaa aggtctctat 1260
cccagcgaca tcgccgtgga gtgggagagc aatgggcagc cggagaacaa ctacaagacc 1320
acgcctcccg tgctggactc cgacggctcc ttcttctct acagcaagct caccgtggac 1380
aagagcaggt ggacgcaggg gaacgtcttc tcatgctccg tgatgcatga ggctctgcac 1440
aaccactaca cgcagaagag cctctccctg tctccgggta aatgatctag a 1491

<210> 339
<211> 1645
<212> DNA
<213> Artificial Sequence

<220>
<223> fusion polynucleotide

<400> 339
aagcttatgg attttcaagt gcagattttc agcttcctgc taatcagtgc ttcagtcata 60
atgtccagag gagtgcacat tgtgtcact cagtctccaa caaccatagc tgcattctcca 120
ggggagaagg tcaccatcac ctgccgtgcc agctccagt taagttacat gtactgggtac 180
cagcagaagt caggcgctc ccctaaactc tggatttatg acacatccaa gctggcttct 240
ggagttccaa atcgcttcag tggcagtggg tctgggacct cttattctct cgcaatcaac 300
accatggaga ctgaagatgc tgccacttat tactgtcagc agtggagtag tactccgctc 360
acgttcgggt ctgggaccaa gctggagatc aaacgggggtg gcggtggctc gggcgggtggt 420
gggtcgggtg gcggcggatc tcaggtgcag ctgaaggagg caggacctgg cctgggtgcaa 480
ccgacacaga ccctgtccct cacatgcact gtctctgggt tctcattaac cagcgaatggt 540
gtacactgga ttcgacagcc tccaggaaag ggtctggaat ggatgggaat aatatattat 600
gatggaggca cagattataa ttcagcaatt aaatccagac tgagcatcag cagggaacacc 660
tccaagagcc aagttttctt aaaaatcaac agtctgcaaa ctgatgacac agccatgtat 720
tactgtgcca gaatccactt tgattactgg ggccaaggag tcatggtcac agtctcctct 780
gatctggagc ccaaactctt tgacaaaact cacacaagcc caccgagccc agcacctgaa 840

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt

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ctcctggggg gatcgtcagt cttcctcttc ccccaaaaac ccaaggacac cctcatgata 900
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aagttcaact ggtacgtgga cggcgtggag gtgcataatg ccaagacaaa gccgcgggag 1020
gagcagtaca acagcacgta ccgtgtggtc agcgtcctca ccgtcctgca ccaggactgg 1080
ctgaatggca aggagtacaa gtgcaaggtc tccaacaaag ccctcccagc ccccatcgag 1140
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cccagcgaca tcgccgtgga gtgggagagc aatgggcagc cggagaacaa ctacaagacc 1320
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ctcccatcct gggccattac cttaattctca gtaaatggaa tttttgtgat atgctgcctg 1560
acctactgct ttgcccgaag atgcagagag agaaggagga atgagagatt gagaagggaa 1620
agtgtacgcc ctgtataaat cgata 1645
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<210> 340
<211> 1645
<212> DNA
<213> Artificial Sequence

<220>
<223> fusion polynucleotide

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<400> 340
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atgtccagag gattcgacat tggctcact cagtctccaa caaccatagc tgcattctca 120
ggggagaagg tcaccatcac ctgccgtgcc agctccagtg taagtacat gtactgggtac 180
cagcagaagt caggcgctc ccctaaactc tggatttatg acacatccaa gctggcttct 240
ggagttccaa atcgcttcag tggcagtggt tctgggacct ctattctctt cgcaatcaac 300
accatggaga ctgaagatgc tgccacttat tactgtcagc agtggagtag tactccgctc 360
acgttcgggt ctgggaccaa gctggagatc aaacgggggt gcggtggctc ggcggtgggt 420
gggtcgggtg gcggcgatc tcaggtgcag ctgaaggagg caggacctgg cctgggtgaa 480
cgcacacaga cctgtccct cacatgcact gtctctgggt tctcattaac cagcgatggt 540
gtacactgga ttgcagagcc tccaggaaag ggtctggaat ggatgggaat aatatattat 600
gatggaggca cagattataa ttcagcaatt aaatccagac tgagcatcag cagggacacc 660
tccaagagcc aagttttctt aaaaatcaac agtctgcaaa ctgatgacac agccatgtat 720
tactgtgcca gaatccactt tgattactgg ggccaaggag tcatgggtcac agtctcctct 780
gatctggagc ccaaactctt tgacaaaact cacacatgcc caccgtgccc agcacctgaa 840
ctcctggggg gaccgtcagt cttcctcttc ccccaaaaac ccaaggacac cctcatgata 900
tcccggaccc ctgaggtcac atgctgtggt gtggacgtga gccacgaaga ccctgaggtc 960
aagttcaact ggtacgtgga cggcgtggag gtgcataatg ccaagacaaa gccgcgggag 1020
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tcccgggatg agctgaccaa gaaccaggtc agcctgacct gcctgggtcaa aggtctctat 1260
cccagcgaca tcgccgtgga gtgggagagc aatgggcagc cggagaacaa ctacaagacc 1320
acgcctcccg tgctggactc cgacggctcc ttcttctctt acagcaagct caccgtggac 1380
aagagcaggt ggcagcaggg gaacgtcttc tcatgtctcc tgatgcatga ggctctgcac 1440
aaccactaca cgcagaagag cctctccctg tctccgggta aagcggatcc ttcgaaacctg 1500
ctcccatcct gggccattac cttaattctca gtaaatggaa tttttgtgat atgctgcctg 1560
acctactgct ttgcccgaag atgcagagag agaaggagga atgagagatt gagaagggaa 1620
agtgtacgcc ctgtataaat cgata 1645
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<210> 341
<211> 113
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion polypeptide

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<400> 341
Gln Val Gln Leu Lys Glu Ala Gly Pro Gly Leu Val Gln Pro Thr Gln
1      5      10      15
Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Ser Asp
20      25      30
Gly Val His Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Met
35      40      45
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49076.000004pct2_10.207.655 Seq List Text 07.24.03.txt
Gly Ile Ile Tyr Tyr Asp Gly Gly Thr Asp Tyr Asn Ser Ala Ile Lys
50 55 60
Ser Arg Leu Ser Ile Ser Arg Asp Thr Ser Lys Ser Gln Val Phe Leu
65 70 75 80
Lys Ile Asn Ser Leu Gln Thr Asp Asp Thr Ala Met Tyr Tyr Cys Ala
85 90 95
Arg Ile His Phe Asp Tyr Trp Gly Gln Gly Val Met Val Thr Val Ser
100 105 110
Ser

<210> 342
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion polypeptide

<400> 342
Asp Ile Val Leu Thr Gln Ser Pro Thr Thr Ile Ala Ala Ser Pro Gly
1 5 10 15
Glu Lys Val Thr Ile Thr Cys Arg Ala Ser Ser Ser Val Ser Tyr Met
20 25 30
Tyr Trp Tyr Gln Gln Lys Ser Gly Ala Ser Pro Lys Leu Trp Ile Tyr
35 40 45
Asp Thr Ser Lys Leu Ala Ser Gly Val Pro Asn Arg Phe Ser Gly Ser
50 55 60
Gly Ser Gly Thr Ser Tyr Ser Leu Ala Ile Asn Thr Met Glu Thr Glu
65 70 75 80
Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Thr Pro Leu Thr
85 90 95
Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys Arg
100 105

<210> 343
<211> 258
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion polypeptide

<400> 343
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
1 5 10 15
Val Ile Met Ser Arg Gly Val Asp Ile Val Leu Thr Gln Ser Pro Thr
20 25 30
Thr Ile Ala Ala Ser Pro Gly Glu Lys Val Thr Ile Thr Cys Arg Ala
35 40 45
Ser Ser Ser Val Ser Tyr Met Tyr Trp Tyr Gln Gln Lys Ser Gly Ala
50 55 60
Ser Pro Lys Leu Trp Ile Tyr Asp Thr Ser Lys Leu Ala Ser Gly Val
65 70 75 80
Pro Asn Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Ala
85 90 95
Ile Asn Thr Met Glu Thr Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln
100 105 110
Trp Ser Ser Thr Pro Leu Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile
115 120 125
Lys Arg Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Gly
130 135 140
Ser Gln Val Gln Leu Lys Glu Ala Gly Pro Gly Leu Val Gln Pro Thr
145 150 155 160
Gln Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Ser
165 170 175
Asp Gly Val His Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
 180 185 190
 Met Gly Ile Ile Tyr Tyr Asp Gly Thr Asp Tyr Asn Ser Ala Ile
 195 200 205
 Lys Ser Arg Leu Ser Ile Ser Arg Asp Thr Ser Lys Ser Gln Val Phe
 210 215 220
 Leu Lys Ile Asn Ser Leu Gln Thr Asp Asp Thr Ala Met Tyr Tyr Cys
 225 230 235 240
 Ala Arg Ile His Phe Asp Tyr Trp Gly Gln Gly Val Met Val Thr Val
 245 250 255
 Ser Ser

<210> 344
 <211> 492
 <212> PRT
 <213> Artificial sequence

<220>
 <223> fusion polypeptide

<400> 344
 Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1 5 10 15
 Val Ile Met Ser Arg Gly Val Asp Ile Val Leu Thr Gln Ser Pro Thr
 20 25 30
 Thr Ile Ala Ser Pro Gly Glu Lys Val Thr Ile Thr Cys Arg Ala
 35 40 45
 Ser Ser Ser Val Ser Tyr Met Tyr Trp Tyr Gln Gln Lys Ser Gly Ala
 50 55 60
 Ser Pro Lys Leu Trp Ile Tyr Asp Thr Ser Lys Leu Ala Ser Gly Val
 65 70 75 80
 Pro Asn Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Ala
 85 90 95
 Ile Asn Thr Met Glu Thr Glu Asp Ala Thr Tyr Tyr Cys Gln Gln
 100 105 110
 Trp Ser Ser Thr Pro Leu Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile
 115 120 125
 Lys Arg Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Gly
 130 135 140
 Ser Gln Val Gln Leu Lys Glu Ala Gly Pro Gly Leu Val Gln Pro Thr
 145 150 155 160
 Gln Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Ser
 165 170 175
 Asp Gly Val His Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp
 180 185 190
 Met Gly Ile Ile Tyr Tyr Asp Gly Thr Asp Tyr Asn Ser Ala Ile
 195 200 205
 Lys Ser Arg Leu Ser Ile Ser Arg Asp Thr Ser Lys Ser Gln Val Phe
 210 215 220
 Leu Lys Ile Asn Ser Leu Gln Thr Asp Asp Thr Ala Met Tyr Tyr Cys
 225 230 235 240
 Ala Arg Ile His Phe Asp Tyr Trp Gly Gln Gly Val Met Val Thr Val
 245 250 255
 Ser Ser Asp Gln Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro
 260 265 270
 Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
 275 280 285
 Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
 290 295 300
 Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
 305 310 315 320
 Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
 325 330 335
 Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
 340 345 350
 Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
 355 360 365
 Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
 370 375 380
 Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
 385 390 395 400
 Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
 405 410 415
 Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
 420 425 430
 Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
 435 440 445
 Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
 450 455 460
 Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
 465 470 475 480
 Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 485 490

<210> 345
 <211> 543
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> fusion polypeptide

<400> 345
 Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1 5 10 15
 Val Ile Met Ser Arg Gly Val Asp Ile Val Leu Thr Gln Ser Pro Thr
 20 25 30
 Thr Ile Ala Ser Pro Gly Glu Lys Val Thr Ile Thr Cys Arg Ala
 35 40 45
 Ser Ser Ser Val Ser Tyr Met Tyr Trp Tyr Gln Gln Lys Ser Gly Ala
 50 55 60
 Ser Pro Lys Leu Trp Ile Tyr Asp Thr Ser Lys Leu Ala Ser Gly Val
 65 70 75 80
 Pro Asn Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Ala
 85 90 95
 Ile Asn Thr Met Glu Thr Glu Asp Ala Thr Tyr Tyr Cys Gln Gln
 100 105 110
 Trp Ser Ser Thr Pro Leu Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile
 115 120 125
 Lys Arg Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Gly
 130 135 140
 Ser Gln Val Gln Leu Lys Glu Ala Gly Pro Gly Leu Val Gln Pro Thr
 145 150 155 160
 Gln Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Ser
 165 170 175
 Asp Gly Val His Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp
 180 185 190
 Met Gly Ile Ile Tyr Tyr Asp Gly Thr Asp Tyr Asn Ser Ala Ile
 195 200 205
 Lys Ser Arg Leu Ser Ile Ser Arg Asp Thr Ser Lys Ser Gln Val Phe
 210 215 220
 Leu Lys Ile Asn Ser Leu Gln Thr Asp Asp Thr Ala Met Tyr Tyr Cys
 225 230 235 240
 Ala Arg Ile His Phe Asp Tyr Trp Gly Gln Gly Val Met Val Thr Val
 245 250 255
 Ser Ser Asp Leu Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro
 260 265 270
 Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
 275 280 285
 Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
 290 295 300
 Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
 305 310 315 320
 Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
 325 330 335
 Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
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 Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
 355 360 365
 Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
 370 375 380
 Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
 385 390 395 400
 Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
 405 410 415
 Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
 420 425 430
 Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
 435 440 445
 Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
 450 455 460
 Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
 465 470 475 480
 Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Ala Asp Pro Ser
 485 490 495
 Asn Leu Leu Pro Ser Trp Ala Ile Thr Leu Ile Ser Val Asn Gly Ile
 500 505 510
 Phe Val Ile Cys Cys Leu Thr Tyr Cys Phe Ala Pro Arg Cys Arg Glu
 515 520 525
 Arg Arg Arg Asn Glu Arg Leu Arg Arg Glu Ser Val Arg Pro Val
 530 535 540

<210> 346
 <211> 543
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> fusion polypeptide

<400> 346
 Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1 5 10 15
 Val Ile Met Ser Arg Gly Val Asp Ile Val Leu Thr Gln Ser Pro Thr
 20 25 30
 Thr Ile Ala Ser Pro Gly Glu Lys Val Thr Ile Thr Cys Arg Ala
 35 40 45
 Ser Ser Ser Val Ser Tyr Met Tyr Trp Tyr Gln Gln Lys Ser Gly Ala
 50 55 60
 Ser Pro Lys Leu Trp Ile Tyr Asp Thr Ser Lys Leu Ala Ser Gly Val
 65 70 75 80
 Pro Asn Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Ala
 85 90 95
 Ile Asn Thr Met Glu Thr Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln
 100 105 110
 Trp Ser Ser Thr Pro Leu Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile
 115 120 125
 Lys Arg Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
 130 135 140
 Ser Gln Val Gln Leu Lys Glu Ala Gly Pro Gly Leu Val Gln Pro Thr
 145 150 155 160
 Gln Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Ser
 165 170 175
 Asp Gly Val His Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp
 180 185 190
 Met Gly Ile Ile Tyr Tyr Asp Gly Gly Thr Asp Tyr Asn Ser Ala Ile
 195 200 205
 Lys Ser Arg Leu Ser Ile Ser Arg Asp Thr Ser Lys Ser Gln Val Phe
 210 215 220
 Leu Lys Ile Asn Ser Leu Gln Thr Asp Asp Thr Ala Met Tyr Tyr Cys
 225 230 235 240
 Ala Arg Ile His Phe Asp Tyr Trp Gly Gln Gly Val Met Val Thr Val
 245 250 255
 Ser Ser Asp Leu Glu Pro Lys Ser Ser Asp Lys Thr His Thr Ser Pro

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
 260 265 270
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 275 280 285
 Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
 290 295 300
 Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
 305 310 315 320
 Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
 325 330 335
 Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
 340 345 350
 Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
 355 360 365
 Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
 370 375 380
 Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
 385 390 395 400
 Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
 405 410 415
 Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
 420 425 430
 Glu Asn Asn Tyr Lys Thr Thr Pro Val Leu Asp Ser Asp Gly Ser
 435 440 445
 Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
 450 455 460
 Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
 465 470 475 480
 Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Ala Asp Pro Ser
 485 490 495
 Asn Leu Leu Pro Ser Trp Ala Ile Thr Leu Ile Ser Val Asn Gly Ile
 500 505 510
 Phe Val Ile Cys Cys Leu Thr Tyr Cys Phe Ala Pro Arg Cys Arg Glu
 515 520 525
 Arg Arg Arg Asn Glu Arg Leu Arg Arg Glu Ser Val Arg Pro Val
 530 535 540

<210> 347
 <211> 1527
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> fusion polynucleotide

<400> 347
 aagcttatgg attttcaagt gcagattttc agcttctctgc taatcagtg c ttcagtcata 60
 atgtccagag gagtcgacat ccagatgaca cagactacat cctccctgtc tgcctctctg 120
 ggagacagag tcaccatcag ttgcagggca agtcaggaca ttcgcaatta tttaaactgg 180
 tatcagcaga aaccagatgg aactgttaaa ctctgatct actacacatc aagattacac 240
 tcaggagtcc catcaagggt cagtggcagt gggctctggaa cagattattc tctcaccatt 300
 gccaacctgc aaccagaaga tattgccact tacttttgcc aacagggtaa tacgcttccg 360
 tggacgttcg gtggaggcac caaactggta accaaacggg agctcggtg cgggtggctcg 420
 ggcggtggtg ggtcgggtgg cggcggatct atcgaatgagg tccagctgca acagcttgga 480
 cctgaactgg tgaagcctgg agcttcaatg tcctgcaagg cctctggta ctcttact 540
 ggctacatcg tgaactggct gaagcagagc catggaaaga accttgagt gattggactt 600
 attaatccat acaaaaggct tactacctac aaccagaaat tcaagggcaa ggccacatta 660
 actgtagaca agtcatccag cacagcctac atggagctcc tcagtctgac atctgaagac 720
 tctgcagtct attactgtgc aagatctggg tactatgggt actcggactg gtacttcgat 780
 gtctggggcg cagggaccac ggtcaccgtc tcctctgate aggagcccaa atcttgtgac 840
 aaaactcaca catgcccacc gtgcccagca cctgaactcc tggggggacc gtcagcttc 900
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 gtgggtgggtg acgtgagcca cgaagaccct gaggtcaagt tcaactggta cgtggacggc 1020
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 aagggtctcca acaaagccct cccagcccc atcgagaaaa caatctccaa agccaaagg 1200
 cagccccgag aaccacaggt gtacaccctg ccccatccc gggatgagct gaccaagaac 1260
 caggtcagcc tgacctgcct ggtcaaaggc ttctatccca gcgacatcg cgtggagtgg 1320
 gagagcaatg ggcagccgga gaacaactac aagaccacgc ctcccgtgct ggactccgac 1380

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
ggctccttct tcctctacag caagctcacc gtggacaaga gcagggtggca gcaggggaac 1440
gtcttctcat gctccgtgat gcatgaggct ctgcacaacc actacacgca gaagagcctc 1500
tcctgtcttc cgggtaaattg atctaga 1527

<210> 348
<211> 504
<212> PRT
<213> Artificial sequence

<220>
<223> fusion polypeptide

<400> 348
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
1 5 10 15
Val Ile Met Ser Arg Gly Val Asp Ile Gln Met Thr Gln Thr Thr Ser
20 25 30
Ser Leu Ser Ala Ser Leu Gly Asp Arg Val Thr Ile Ser Cys Arg Ala
35 40 45
Ser Gln Asp Ile Arg Asn Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Asp
50 55 60
Gly Thr Val Lys Leu Leu Ile Tyr Tyr Thr Ser Arg Leu His Ser Gly
65 70 75 80
Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu
85 90 95
Thr Ile Ala Asn Leu Gln Pro Glu Asp Ile Ala Thr Tyr Phe Cys Gln
100 105 110
Gln Gly Asn Thr Leu Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Val
115 120 125
Thr Lys Arg Glu Leu Gly Gly Gly Ser Gly Gly Gly Ser Gly
130 135 140
Gly Gly Gly Ser Ile Asp Glu Val Gln Leu Gln Gln Ser Gly Pro Glu
145 150 155 160
Leu Val Lys Pro Gly Ala Ser Met Ser Cys Lys Ala Ser Gly Tyr Ser
165 170 175
Phe Thr Gly Tyr Ile Val Asn Trp Leu Lys Gln Ser His Gly Lys Asn
180 185 190
Leu Glu Trp Ile Gly Leu Ile Asn Pro Tyr Lys Gly Leu Thr Thr Tyr
195 200 205
Asn Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser
210 215 220
Ser Thr Ala Tyr Met Glu Leu Leu Ser Leu Thr Ser Glu Asp Ser Ala
225 230 235 240
Val Tyr Tyr Cys Ala Arg Ser Gly Tyr Tyr Gly Asp Ser Asp Trp Tyr
245 250 255
Phe Asp Val Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ser Asp Gln
260 265 270
Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
275 280 285
Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
290 295 300
Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
305 310 315 320
Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
325 330 335
Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
340 345 350
Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
355 360 365
Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
370 375 380
Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
385 390 395 400
Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
405 410 415
Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
420 425 430
Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
435 440 445

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
 Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
 450 455 460
 Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
 465 470 475 480
 Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
 485 490 495
 Ser Leu Ser Leu Ser Pro Gly Lys
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<210> 349
 <211> 2325
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> fusion polynucleotide

<400> 349
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 gtcataattg ccagaggaca aattgttctc tcccagctctc cagcaatcct gtctgcatct 120
 ccaggggaga aggtcacaaat gacttgcagg gccagctcaa gtgtaagtta catgcaactg 180
 taccagcaga agccaggatc ctccccaaa ccctggattt atgccccatc caacctggct 240
 tctggagtcc ctgctcgctt cagtggcagt gggctctggga cctcttactc tctcacaatc 300
 agcagagtgg aggtgaaga tgctgccact tattactgcc agcagtggag tttaaccca 360
 cccacgttcg gtgctgggac caagctggag ctgaaagggt gcggtggctc gggcggtggg 420
 ggatctggag gaggtgggag ctctcaggct tatctacagc agtctggggc tgagctgggt 480
 aggcctgggg cctcagtga gatgtcctgc aaggcttctg gctacacatt taccagttac 540
 aatattgcact gggtaaagca gacacctaga cagggcctgg aatggattgg agctatttat 600
 ccaggaaatg gtgatacttc ctacaatcag aagttcaagg gcaaggccac actgactgta 660
 gacaaatcct ccagcacagc ctacatgcag ctacagagcc tgacatctga agactctgcg 720
 gtctatttct gtgcaagagt ggtgtactat agtaactctt actggtactt cgatgtctgg 780
 ggcacaggga ccacggtcac cgtctcttct gatcaatcca actctgaaga agcaaagaaa 840
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 tctccagcca ccctgtctgt gactccagga gactagagtct ctctttctcg cagggccagc 960
 cagagtatta gcgactactt acactgggtat caacaaaaat cacatgagtc tccaaggctt 1020
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 tcagggtcag atttcactct cagtatcaac agtgtggaac ctgaagatgt tgggaatttat 1140
 tactgtcaac atggtcacag ctttccgtgg acgttccgtg gaggcaccaa gctggaaatc 1200
 aaacgggggt gcggtggctc gggcgagggt gggctcgggtg gcggcggtat tcagatccag 1260
 ttggtgcaat ctggacctga gctgaagaag cctggagaga cagtcaggat ctctgcaag 1320
 gcttctgggt atgccttcac aactactgga atgcagtggg tgcaagagat gccaggaaaag 1380
 ggtttgaagt ggattggctg gataaacacc ccactctgga gtgccaaaat atgtagaaga 1440
 cttcaaggac ggtttgctt ctctttggaa acctctgcca acactgcata ttacagata 1500
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 tacaacagca cgtaccgtgt ggtcagcgtc ctaccgtcc tgcaccagga ctggctgaat 1920
 ggcaaggagt acaagtcaa ggtctccaac aaagccctcc cagccccat cgagaaaaca 1980
 atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg 2040
 gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatcccagc 2100
 gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgct 2160
 cccgtgctgg actccgacgg ctcttcttct ctctacagca agctcacct ggacaagagc 2220
 aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac 2280
 tacacgcaga agagcctctc cctgtctccg ggtaaatgat ctaga 2325

<210> 350
 <211> 768
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> fusion polypeptide

<400> 350
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35      40      45
Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser
50      55      60
Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro
65      70      75      80
Ala Arg Phe Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
85      90      95
Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
100      105      110
Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
115      120      125
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser
130      135      140
Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala
145      150      155      160
Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
165      170      175
Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile
180      185      190
Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
195      200      205
Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Thr Ala Tyr
210      215      220
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
225      230      235      240
Ala Arg Val Val Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp
245      250      255
Gly Thr Gly Thr Thr Val Thr Val Ser Ser Asp Gln Ser Asn Ser Glu
260      265      270
Glu Ala Lys Lys Glu Glu Ala Lys Glu Glu Ala Lys Lys Ser Asn
275      280      285
Ser Val Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Val Thr
290      295      300
Pro Gly Asp Arg Val Ser Leu Ser Cys Arg Ala Ser Gln Ser Ile Ser
305      310      315
Asp Tyr Leu His Trp Tyr Gln Gln Lys Ser His Glu Ser Pro Arg Leu
320      325      330      335
Leu Ile Lys Tyr Ala Ser His Ser Ile Ser Gly Ile Pro Ser Arg Phe
340      345      350
Ser Gly Ser Gly Ser Gly Ser Asp Phe Thr Leu Ser Ile Asn Ser Val
355      360      365
Glu Pro Glu Asp Val Gly Ile Tyr Tyr Cys Gln His Gly His Ser Phe
370      375      380
Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg Gly Gly
385      390      395      400
Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gln Ile Gln
405      410      415
Leu Val Gln Ser Gly Pro Glu Leu Lys Lys Pro Gly Glu Thr Val Arg
420      425      430
Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Thr Thr Gly Met Gln
435      440      445
Trp Val Gln Glu Met Pro Gly Lys Gly Leu Lys Trp Ile Gly Trp Ile
450      455      460
Asn Thr Pro Leu Trp Ser Ala Lys Ile Cys Arg Arg Leu Gln Gly Arg
465      470      475      480
Phe Ala Phe Ser Leu Glu Thr Ser Ala Asn Thr Ala Tyr Leu Gln Ile
485      490      495
Ser Asn Leu Lys Asp Glu Asp Thr Ala Thr Tyr Phe Cys Val Arg Ser
500      505      510
Gly Asn Gly Asn Tyr Asp Leu Ala Tyr Phe Ala Tyr Trp Gly Gln Gly
515      520      525
Thr Leu Val Thr Val Ser Asp Gln Glu Pro Lys Ser Ser Asp Lys Thr
530      535      540
His Thr Ser Pro Pro Ser Pro Ala Pro Glu Leu Leu Gly Gly Ser Ser
545      550      555      560

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565 570 575
Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
580 585 590
Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
595 600 605
Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
610 615 620
Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
625 630 635 640
Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr
645 650 655
Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
660 665 670
Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys
675 680 685
Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
690 695 700
Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
705 710 715 720
Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
725 730 735
Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
740 745 750
Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
755 760 765

<210> 351
<211> 1521
<212> DNA
<213> Artificial Sequence

<220>
<223> fusion polynucleotide

<400> 351
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gtcataattg ccagaggaca aattgtttct tcccagctct cagcaatect gtctgcatct 120
ccaggggaga aggtcacaat gacttgcagg gccagctcaa gtgtaagtta catgcactgg 180
taccagcaga agccaggatc ctcccccaa ccctggattt atgccccatc caacctggct 240
tctggagtc ctgctcgctt cagtggcagt gggctctggga cctcttactc tctcacaatc 300
agcagagtgg aggtgaaaga tgctgccact tattactgcc agcagtgagg ttttaaccca 360
cccacgttcg gtgctgggac caagctggag ctgaaagatg gcggtggctc gggcggtggt 420
ggatctggag gaggtgggag ctctcaggct tatctacagc agtctggggc tgagctggtg 480
aggcctgggg cctcagtga gatgtctgc aaggcttctg gctacacatt taccagttac 540
aatatgcact gggtaaagca gacacctaga cagggcctgg aatggattgg agctatttat 600
ccaggaaatg gtgatacttc ctacaatcag aagttcaagg gcaaggccac actgactgta 660
gacaaatcct ccagcacagc ctacatgcag ctacagagcc tgacatctga agactctgcg 720
gtctatttct gtgcaagagt ggtgtactat agtaactctt actggtactt cgatgtctgg 780
ggcacagggg ccacggtcac cgtctcttct gatcaggagc ccaaatcttc tgacaaaact 840
cacacatccc caccgtcccc agcacctgaa ctctggggg gatcgtcagt cttcctcttc 900
ccccaaaac ccaaggacac cctcatgata tcccggacc ctgaggtcac atgctgtggtg 960
gtggacgtga gccacgaaga cctgaggtc aagttcaact ggtacgtgga cggcgtggag 1020
gtgcataatg ccaagacaaa gccgcgggag gagcagtaca acagcacgta ccgtgtgggtc 1080
agcgtcctca ccgtcctgca ccaggactgg ctgaatggca aggagtacaa gtgcaaggtc 1140
tccaacaaag cctccccagc ccccatcgag aaaacaatct ccaaagccaa agggcagccc 1200
cgagaaccac aggtgtacac cctgccccca tcccgggatg agctgaccaa gaaccagggtc 1260
agcctgacct gcctgggtcaa aggttcttat ccagcgaca tcgctgggta gtgggagagc 1320
aatgggcagc cggagaacaa ctacaagacc acgctctccg tgctggactc cgacggctcc 1380
ttcttctctt acagcaagct caccgtggac aagagcaggt ggcagcaggg gaacgtcttc 1440
tcatgctccg tgatgcatga ggctctgcac aaccactaca cgcagaagag cctctccctg 1500
tctccgggta aatgatctag a 1521

<210> 352
<211> 500
<212> PRT
<213> Artificial Sequence

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<220>

<223> fusion polypeptide

<400> 352

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Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
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Val Ile Ile Ala Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile
 20      25      30
Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser
 35      40      45
Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser
 50      55      60
Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro
 65      70      75
Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
 80      85      90
Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
 95      100      105
Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
 110      115      120
Asp Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Ser
 125      130      135
Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala
 140      145      150
Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
 155      160      165
Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile
 170      175      180
Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
 185      190      195
Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Thr Ala Tyr
 200      205      210
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
 215      220      225
Ala Arg Val Val Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp
 230      235      240
Gly Thr Gly Thr Thr Val Thr Val Ser Ser Asp Gln Glu Pro Lys Ser
 245      250      255
Ser Asp Lys Thr His Thr Ser Pro Ser Pro Ala Pro Glu Leu Leu
 260      265      270
Gly Gly Ser Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
 275      280      285
Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Asp Val Ser
 290      295      300
His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
 305      310      315
Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
 320      325      330
Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
 335      340      345
Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
 350      355      360
Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
 365      370      375
Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
 380      385      390
Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
 395      400      405
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
 410      415      420
Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
 425      430      435
Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
 440      445      450
Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
 455      460      465
Ser Pro Gly Lys
 470      475      480
                    485      490      495
                    500

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<210> 353
<211> 423
<212> DNA
<213> Artificial Sequence

<220>
<223> fusion polynucleotide

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tgcacagtct ctggtttctc attaaactacc tatgctgtac actgggttcg ccagtcctca 180
ggaaagggtc tggagtggtt gggagtgata tggagtggtg gaatcacaga ctataatgca 240
gctttcatat ccagactgag catcaccaag gacgattcca agagccaagt tttctttaaa 300
atgaacagtc tgcaacctaa tgacacagcc atttattact gtgccagaaa tgggggtgat 360
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tca 423

<210> 354
<211> 366
<212> DNA
<213> qArtificial Sequence

<220>
<223> fusion polynucleotide

<400> 354
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acctgcacag tctctgggtt ctcattaact acctatgctg tacactgggt tcgccagtct 120
ccaggaaagg gtctggagtg gctgggagtg atatggagtg gtggaatcac agactataat 180
gcagctttca tatccagact gagcatcacc aaggacgatt ccaagagcca agttttcttt 240
aaaatgaaca gtctgcaacc taatgacaca gccatttatt actgtgccag aaatgggggt 300
gataactacc cttattacta tgctatggac tactgggggtc aaggaaacctc agtcaccgtc 360
tcctca 366

<210> 355
<211> 399
<212> DNA
<213> Artificial Sequence

<220>
<223> fusion polynucleotide

<400> 355
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gatattgtga tgacgcaggc tgcattctcc aatccagtc cttctggaac atcagcttcc 120
atctcctgca ggtctagtaa gagtctccta catagtaatg gcatcactta tttgtattgg 180
tatctgcaga agccaggcca gtctcctcag ctccgtgatt atcagatgtc caaccttgcc 240
tcaggagtc cagacagggt cagtagcagt gggtcaggaa ctgatttcac actgagaatc 300
agcagagtgg aggctgagga tgtgggtgtt tattactgtg ctcaaaatct agaacttccg 360
ctcacgttcg gtgctgggac caagctggag ctgaaacgg 399

<210> 356
<211> 825
<212> DNA
<213> Artificial Sequence

<220>
<223> fusion polynucleotide

<400> 356
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ggatccactg cagatattgt gatgacgcag gctgcattct ccaatccagt cactcttgga 120
acatcagctt ccatctcctg caggctcagt aagagtctcc tacatagtaa tggcatcact 180
tatttgattt ggtatctgca gaagccaggc cagctccttc agctcctgat ttatcagatg 240
tccaaccttg cctcaggagt cccagacagg ttcagtagca gtgggtcagg aactgatttc 300
acactgagaa tcagcagagt ggaggctgag gatgtgggtg tttattactg tgctcaaaat 360
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